GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 3, 2006, 05:30:20 ; Search time 23 Seconds
(without alignments)
1008.184 Million cell updates/sec

Title: US-09-979-539-1
Perfect score: 1276
Sequence: 1 MQVQLQQSGPELEKPGASVK.....CQQWSGYPLTFGAGTKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	850.5	66.7	268	2	A56446	Ig heavy chain V r
2	733	57.4	249	2	S41374	single chain Fv an
3	663	52.0	233	2	JC5322	p53 specific singl
4	529	41.5	144	2	B30502	Ig heavy chain V r
5	516.5	40.5	122	2	PH0887	Ig heavy chain V r
6	513.5	40.2	137	2	H32513	Ig heavy chain pre
7	503.5	39.5	120	2	E45722	anti-glycoprotein
8	502	39.3	130	1	JL0079	Ig kappa chain pre
9	501.5	39.3	119	2	F30502	Ig heavy chain V r
10	501	39.3	119	2	PH0099	Ig heavy chain V r
11	500.5	39.2	114	2	S26319	Ig heavy chain V r
12	499	39.1	103	2	S29591	Ig kappa chain V r
13	499	39.1	107	2	A30562	Ig kappa chain V r
14	496.5	38.9	120	2	F45722	anti-glycoprotein
15	496	38.9	107	2	B30562	Ig kappa chain V r
16	496	38.9	107	2	PC4405	Ig kappa chain V r
17	495.5	38.8	135	2	PS0057	Ig heavy chain pre
18	495	38.8	104	2	B49049	Ig kappa chain V r
19	495	38.8	106	2	PS0071	Ig kappa chain V r
20	495	38.8	235	2	S25058	Ig kappa chain - m
21	493.5	38.7	128	2	I37267	Ig heavy chain V r
22	492.5	38.6	118	1	MHMS38	Ig heavy chain V r
23	491.5	38.5	128	2	C37267	Ig heavy chain V r
24	487	38.2	119	2	B53285	Ig heavy chain V a
25	487	38.2	125	2	PH0100	Ig heavy chain V r
26	482.5	37.8	139	2	A27609	Ig heavy chain pre
27	482	37.8	107	2	S11119	Ig kappa chain V r
28	482	37.8	107	2	PT0398	Ig light chain V r
29	481.5	37.7	112	2	S09957	Ig heavy chain V-D
30	481	37.7	107	2	S11118	Ig kappa chain V r
31	478	37.5	107	2	PT0402	Ig light chain V r
32	478	37.5	107	2	S11121	Ig kappa chain V r
33	478	37.5	117	1	MHMS4E	Ig heavy chain V r
34	478	37.5	117	1	MHMSJ5	Ig heavy chain V r
35	478	37.5	140	2	T01407	Ig heavy chain (my
36	475	37.2	106	2	G27887	Ig kappa chain V r
37	474	37.1	107	2	PD0011	Ig kappa chain V r
38	474	37.1	120	2	A34871	Ig kappa chain V r
39	473.5	37.1	108	2	G30560	Ig kappa chain V r
40	473	37.1	107	2	PT0406	Ig kappa chain V r
41	472.5	37.0	120	2	A49982	Ig heavy chain V r
42	472.5	37.0	128	2	A37267	Ig heavy chain V r
43	472	37.0	107	2	PT0403	Ig light chain V r
44	471	36.9	118	2	PL0200	anti-DNA autoantib
45	470	36.8	100	2	S29590	Ig kappa chain V r

ALIGNMENTS

RESULT 1
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally iden
A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: UNIPARC:UPI000017C6D0; GB:U20617
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.7%; Score 850.5; DB 2; Length 268;
Best Local Similarity 69.6%; Pred. No. 4.6e-49;
Matches 167; Conservative 25; Mismatches 47; Indels 1; Gaps 1;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|| || |||||||||| ||::  |:||||  : ||||| | | ||: |
Db          3 QVKLQESGAELVKPGASVKLSCTTSGFNIKDTYMHWVKQRPEQGLEWIGRIAPANGITKY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              : ||:||||:  | ||:|||: | ||||||:|||:||   |  |  :|||||||||||||
Db         63 DPKFQGKATIAADTSSNTAYLQLSSLTSEDTAVYYCA-SYYLTRYENYWGQGTTVTVSSG 121

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              ||||||  |||||||||||||||||||| ||||||:| |||||::::||||||  ||| |
Db        122 GGGSGGGDSGGGGSDIELTQSPAIMSASLGEKVTMSCRASSSVNFIYWYQQKSDASPKLW 181

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              :| || |  ||| |||||||||||||||||:| || |||||||::  | |||:|||||||
Db        182 VYYTSHLPPGVPARFSGSGSGNSYSLTISSMEGEDAATYYCQQFTSSPFTFGSGTKLEIK 241
```

RESULT 2
S41374
single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: S41374
R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of a single chain Fv antib
A;Reference number: S41374
A;Accession: S41374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>

```
A;Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

  Query Match             57.4%;  Score 733;  DB 2;  Length 249;
  Best Local Similarity   60.6%;  Pred. No. 2.2e-41;
  Matches  149;  Conservative   27;  Mismatches   64;  Indels    6;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              |||||||| || :|||||||||| |||::|    ::||||    | ||||  | | :|    |
Db          1 QVQLQQSGAELVRPGASVKLSCTASGFNFKDDYIHWVKQRPEKGLEWIARIAPASGNVKY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
                :|: |||:| | ||:|||: | |||||||:|||:|||          |||||:||||||
Db         61 VPRFQDKATITADTSSNTAYLLLSSLTSEDTAVYYCARRDTLYTSLGYWGQGSTVTVSSR 120

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV------SYMHWYQQKSG 175
              ||||||||||||||||||||  :   ||| |:::| :| |:      ||: |: |: |
Db        121 GGGSGGGGSGGGGSDIELTQSPPSVVVIPGESVSISCRSSKSLLYSDGDSYLFWFLQRPG 180

Qy        176 TSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAG 235
              ||:  ||  | |||||| |||||||| |::| || |||||   ||| |   ||||||||
Db        181 QSPQLLIYRMSNLASGVPDRFSGSGSGTSFTLRISRVEAEDVGVYYCMQHREYPLTFGAG 240

Qy        236 TKLEIK 241
              ||||:|
Db        241 TKLELK 246


RESULT 3
JC5322
p53 specific single-chain antibody Pab421 - human
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Cross-references: UNIPARC:UPI000017C2DE
A;Experimental source: hydricloma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

  Query Match             52.0%;  Score 663;  DB 2;  Length 233;
  Best Local Similarity   57.5%;  Pred. No. 8.1e-37;
  Matches  138;  Conservative   24;  Mismatches   66;  Indels   12;  Gaps    3;

Qy          6 QQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYNQKF 65
              |:|| || : |||||||  ||::   | |:|||:   : |||| | | || :   :
Db          1 QESGAELVRSGASVKLSCTTSGFNINDYYMHWVKKRPEQGLEWIGRIDPENGDADMTRSS 60

Qy         66 RGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGVGGS 125
                |||:| | ||:|||: | ||||||:|||:|        | |||||||||||| |||
Db         61 GVKATMTADTSSNTAYLQLSSLTSEDTAVYYC------NAGMDYWGQGTTVTVSSGGGGS 114

Qy        126 GGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-----SYMHWYQQKSGTSPKR 180
              ||  |||||||||||||| :: | |:: |::| || ||     ||||| ||| |   |:
Db        115 GGRASGGGGSDIELTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWNQQKPGQPPRL 174

Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
              ||  | | |||| ||||||||  ::| |  || || ||||||      : | ||||||
Db        175 LIYLVSNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHIRELTRSEG-GTKLEI 233


RESULT 4
B30502
Ig heavy chain V region (D444) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Accession: B30502
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mi
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: B30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-144 <EIL>
A;Cross-references: UNIPARC:UPI0000176D4C
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             41.5%;  Score 529;  DB 2;  Length 144;
  Best Local Similarity   63.2%;  Pred. No. 3.1e-28;
  Matches  103;  Conservative   16;  Mismatches   22;  Indels   22;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|||||||||| |||||||:|||||||: ||| |:|||| |: | ||| | |||  : |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTITGYVMHWVKQRPGQGLAWIGYINPYNDGTKY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
                |:||:|||||| |||||||| :| || ||||| |:||||     ||||||||||:||
Db         61 NEKFKGKATLTSDKSSSTAYTELSSLASEDSAAYYCARG-----GFDYWGQGTTLTV--- 112

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV 164
                              || |||||||:| ||||:|: :| || |:
Db        113 --------------DILLTQSPAILSVSPGERVSFSCRASQSI 141


RESULT 5
PH0887
Ig heavy chain V region (anti-CD3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0887
R;Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann
J. Exp. Med. 175, 217-225, 1992
A;Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphoc
A;Reference number: PH0885; MUID:92113462; PMID:1346155
A;Accession: PH0887
A;Molecule type: mRNA
A;Residues: 1-122 <SHA>
A;Cross-references: UNIPARC:UPI0000176B39
A;Note: the authors translated the codon TTC for residue 70 as Leu
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             40.5%;  Score 516.5;  DB 2;  Length 122;
  Best Local Similarity   80.3%;  Pred. No. 1.7e-27;
  Matches   98;  Conservative    9;  Mismatches   12;  Indels    3;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|||||||||| |||||:|:|||||||||||||||||||||||:|||:||| || | |:|
Db          1 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRG---FDYWGQGTTVTV 118
              ||||: ||| |||||||||||:||||||||||||:||| || |     || || ||||||
Db         61 NQKFKDKATFTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 120

Qy        119 SS 120
              ||
Db        121 SS 122


RESULT 6
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.,
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization an
```

A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Cross-references: UNIPARC:UPI0000114D9A; GB:M20831; NID:g196949; PIDN:AAA38848.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 40.2%; Score 513.5; DB 2; Length 137;
Best Local Similarity 82.4%; Pred. No. 3.1e-27;
Matches 98; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ::|||||| || |||||||:|||||||||||| |||||||||||||| | || |::||
Db         20 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGNINPYYGSTSY 79

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              ||||:|||||||||||||| | |||||||||||:|||  | |  |||||||||:||||
Db         80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARKNY-GSSFDYWGQGTTLTVSS 137
```

RESULT 7
E45722
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 5) - mouse (fra
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: E45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A;Reference number: A45722; MUID:93100833; PMID:7677958
A;Accession: E45722
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-120 <SIM>
A;Cross-references: UNIPARC:UPI0000176D4E
A;Note: sequence extracted from NCBI backbone (NCBIP:120593)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 503.5; DB 2; Length 120;
Best Local Similarity 79.2%; Pred. No. 1.2e-26;
Matches 95; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGL-ITPYNGASS 60
              :|||||||||| |||||:|:||||| |||||||||||||||::|||||| | |||| :|
Db          1 EVQLQQSGPELVKPGASMKISCKASVYSFTGYTMNWVKQSHGQNLEWIGLIINPYNGGTS 60

Qy         61 YNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              |||||:||||||||||:||||:|||||| |||||:| | |:     |||||||:|||||
Db         61 YNQKFKGKATLTVDKSSNTAYMELLSLTSADSAVYYCTRRGFRDYSMDYWGQGTSVTVSS 120
```

RESULT 8
JL0079
Ig kappa chain precursor V region (anti-phenyloxazolone 6F6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C;Accession: JL0079; A49044; B49044
R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A;Reference number: JL0076; MUID:89096973; PMID:3211160
A;Accession: JL0079
A;Molecule type: mRNA
A;Residues: 1-130 <KAA>
A;Cross-references: UNIPARC:UPI000017371F; GB:M27792; NID:g197159
A;Experimental source: mRNA clones for anti-phenyloxazolone antibody 6F6
A;Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10
A;Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation
R;Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A;Title: Non-random features of the repertoire expressed by the members of one V kappa
A;Reference number: A49044; MUID:92289826; PMID:1601044
A;Accession: A49044
A;Molecule type: DNA
A;Residues: 1-25 <MIL>
A;Cross-references: UNIPARC:UPI000011760C; GB:S37663; NID:g250214; PIDN:AAB22331.1; PI
A;Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
A;Accession: B49044
A;Molecule type: DNA
A;Residues: 114-116 <MIL2>
A;Cross-references: UNIPARC:UPI000011E8E5; GB:S37664; NID:g250215; PIDN:AAB22332.1; PI
A;Experimental source: BALB/c germ-line
A;Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 add
A;Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)
C;Genetics:
A;Gene: V(kappa)Ox1
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
F;45-109/Disulfide bonds: #status predicted

Query Match 39.3%; Score 502; DB 1; Length 130;
Best Local Similarity 92.4%; Pred. No. 1.6e-26;
Matches 97; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

```
Qy        137 IELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRF 196
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 83

Qy        197 SGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              |||||| |||||||||:|||| |||||||||  |||||||||| |
Db         84 SGSGSGXSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLEXK 128
```

RESULT 9
F30502
Ig heavy chain V region (A52) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Accession: F30502
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: F30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <EIL>
A;Cross-references: UNIPARC:UPI0000176B33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 501.5; DB 2; Length 119;
Best Local Similarity 78.9%; Pred. No. 1.6e-26;
Matches 97; Conservative 9; Mismatches 8; Indels 9; Gaps 2;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ::|||||| || |||||||:|||||||||||| |||||||||||||| | || |::||
Db          1 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGKINPYYGSTSY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCA-----RGGYDGRGFDYWGQGTTV 116
              ||||:|:|||||||||||| | ||||||||||:||     ||||    |||||||||:
Db         61 NQKFKGQATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGRLRRGGY----FDYWGQGTTL 116

Qy        117 TVS 119
              |||
```

```
Db        117 TVS 119


RESULT 10
PH0099
Ig heavy chain V region (anti-cyclosporin F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C;Accession: PH0099
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V
Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A;Reference number: PH0087; MUID:91042649; PMID:2122240
A;Accession: PH0099
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPARC:UPI0000176B47
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;50-66/Region: complementarity-determining 2
F;99-106/Region: complementarity-determining 3

  Query Match             39.3%;  Score 501;  DB 2;  Length 119;
  Best Local Similarity   80.7%;  Pred. No. 1.7e-26;
  Matches   96;  Conservative   11;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|||||||||| :||||:|:||||||||| |||| ||||||||:||||||| ||:|: :
Db          1 EVQLQQSGPELVEPGASMKISCKASGYSFAGYTMIWVKQSHGKNLEWIGLINPYDGSIAT 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              ||||:||||||||||||||||||||||||||:|||| |     |||||||:|||||
Db         61 NQKFKGKATLTVDKSSSTAYMDLLSLTSEDSAVYYCARGYY--YAVDYWGQGTSVTVSS 117


RESULT 11
S26319
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26319
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26319
A;Molecule type: mRNA
A;Residues: 1-114 <STA>
A;Cross-references: UNIPARC:UPI00001769A8; EMBL:X59172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;11-94/Domain: immunoglobulin homology <IMM>

  Query Match             39.2%;  Score 500.5;  DB 2;  Length 114;
  Best Local Similarity   82.6%;  Pred. No. 1.8e-26;
  Matches   95;  Conservative    8;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          6 QQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYNQKF 65
              ||||||| |||||||:|||||||||||| |||||||||||||| | |||| : |||||
Db          1 QQSGPELVKPGASVKISCKASGYSFTGYFMNWVKQSHGKSLEWIGRINPYNGDTFYNQKF 60

Qy         66 RGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              :|||||||||||||:|:||||||||||||:| : || |    |||||||:|||||
Db         61 KGKATLTVDKSSSTAHMELLSLTSEDSAVYYCGKDGYYG-AMDYWGQGTSVTVSS 114


RESULT 12
S29591
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29591
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S29591
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <KAV>
A;Cross-references: UNIPARC:UPI0000115F57; EMBL:X59094; NID:g52227; PIDN:CAA41820.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-88/Domain: immunoglobulin homology <IMM>

  Query Match             39.1%;  Score 499;  DB 2;  Length 103;
  Best Local Similarity   93.2%;  Pred. No. 2e-26;
  Matches   96;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        137 IELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRF 196
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 60

Qy        197 SGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
              |||||| |||||||:|||| |||||||||  |||||||||||
Db         61 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 103


RESULT 13
A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: A30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-b
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: A30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <SIK>
A;Cross-references: UNIPARC:UPI00001767B0
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

  Query Match             39.1%;  Score 499;  DB 2;  Length 107;
  Best Local Similarity   91.4%;  Pred. No. 2.1e-26;
  Matches   96;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        137 IELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRF 196
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          2 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 61

Qy        197 SGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              |||||| |||||||:|||| |||||||||  | ||| |||||||
Db         62 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPYTFGGGTKLEIK 106


RESULT 14
F45722
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 33) - mouse (f
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: F45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vas
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A;Reference number: A45722; MUID:93100833; PMID:7677958
A;Accession: F45722
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-120 <SIM>
A;Cross-references: UNIPARC:UPI0000176D4D
```

```
A;Note: sequence extracted from NCBI backbone (NCBIP:120594)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             38.9%;  Score 496.5;  DB 2;  Length 120;
  Best Local Similarity   78.3%;  Pred. No. 3.5e-26;
  Matches   94;  Conservative   11;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGL-ITPYNGASS 60
              :|||||||||| ||||:|:|||||||||||||||||| ||||:||||| | | || :|
Db          1 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQRHGKSIEWIGLIINPNNGGTS 60

Qy         61 YNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              |||:|||| |||:|||||| ||:||||||||||||:||| |:     | |||||:|||||
Db         61 YNQRFRGKTTLTLDKSSSTVYMELLSLTSEDSAVYYCARRGFRDYALDSWGQGTSVTVSS 120


RESULT 15
B30562
Ig kappa chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: B30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: B30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <SIK>
A;Cross-references: UNIPARC:UPI00001767BA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

  Query Match             38.9%;  Score 496;  DB 2;  Length 107;
  Best Local Similarity   90.5%;  Pred. No. 3.3e-26;
  Matches   95;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        137 IELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRF 196
              | ||||||||||||||||||||||||||||||||||||||||:|||||||||||  ||
Db          2 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWVYDTSKLASGVPTRF 61

Qy        197 SGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              |||||| ||||||||:|||| |||||||||  | ||| |||||||
Db         62 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPYTFGGGTKLEIK 106


Search completed: April  3, 2006, 05:30:51
Job time : 23 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 3, 2006, 05:30:20 ; Search time 56 Seconds
(without alignments)
3036.291 Million cell updates/sec

Title: US-09-979-539-1
Perfect score: 1276
Sequence: 1 MQVQLQQSGPELEKPGASVK.....CQQWSGYPLTFGAGTKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	792.5	62.1	243	2	Q7TQM2_MOUSE	Q7tqm2 mus musculu
2	783.5	61.4	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
3	771.5	60.5	487	2	Q65ZL2_9MURI	Q65zl2 mus sp. fv/
4	733.5	57.5	255	2	Q6KB05_MOUSE	Q6kb05 mus musculu
5	726.5	56.9	241	2	Q921A6_MOUSE	Q921a6 mus musculu
6	718.5	56.3	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
7	645	50.5	248	2	Q65ZQ7_9MURI	Q65zq7 mus sp. b3(
8	628	49.2	218	2	Q925S1_MOUSE	Q925s1 mus musculu
9	543	42.6	170	2	Q925S2_MOUSE	Q925s2 mus musculu
10	514.5	40.3	470	2	Q7TMK1_MOUSE	Q7tmk1 mus musculu
11	502.5	39.4	472	2	Q6PJA7_MOUSE	Q6pja7 mus musculu
12	497	38.9	483	2	Q4VAB6_MOUSE	Q4vab6 mus musculu
13	496	38.9	112	2	Q8K1F0_MOUSE	Q8k1f0 mus musculu
14	496	38.9	235	2	Q58EV6_MOUSE	Q58ev6 mus musculu
15	495.5	38.8	488	2	Q91WR1_MOUSE	Q91wr1 mus musculu
16	492.5	38.6	118	1	HV51_MOUSE	P06330 mus musculu
17	491	38.5	107	1	KV6F_MOUSE	P04940 mus musculu
18	486	38.1	107	1	KV6I_MOUSE	P04943 mus musculu
19	486	38.1	117	2	Q9QXE9_MOUSE	Q9qxe9 mus musculu
20	485	38.0	107	1	KV6H_MOUSE	P04942 mus musculu
21	485	38.0	120	2	Q920E8_MOUSE	Q920e8 mus musculu
22	484	37.9	107	1	KV6G_MOUSE	P04941 mus musculu
23	483	37.9	117	2	Q9QXF0_MOUSE	Q9qxf0 mus musculu
24	482	37.8	134	2	Q8VDD0_MOUSE	Q8vdd0 mus musculu
25	481.5	37.7	481	2	Q8VCV5_MOUSE	Q8vcv5 mus musculu
26	480	37.6	107	1	KV6J_MOUSE	P04944 mus musculu
27	478	37.5	117	1	HV12_MOUSE	P01756 mus musculu
28	478	37.5	117	1	HV13_MOUSE	P01757 mus musculu
29	473	37.1	134	2	Q65ZR6_MOUSE	Q65zr6 mus musculu
30	472.5	37.0	473	2	Q9D8L4_MOUSE	Q9d8l4 mus musculu
31	472.5	37.0	477	2	Q58E56_MOUSE	Q58e56 mus musculu
32	469.5	36.8	458	2	Q5BJZ2_RAT	Q5bjz2 rattus norv
33	468.5	36.7	485	2	Q58E61_MOUSE	Q58e61 mus musculu
34	468	36.7	112	2	Q8K1F2_MOUSE	Q8k1f2 mus musculu
35	467.5	36.6	468	2	Q569W9_MOUSE	Q569w9 mus musculu
36	467	36.6	465	2	Q6PJB2_MOUSE	Q6pjb2 mus musculu
37	466	36.5	123	2	Q8VIJ1_MOUSE	Q8vij1 mus musculu
38	462.5	36.2	598	2	Q568Y0_RAT	Q568y0 rattus norv
39	462	36.2	136	1	HV15_MOUSE	P01759 mus musculu
40	459	36.0	481	2	Q91WT1_MOUSE	Q91wt1 mus musculu
41	457	35.8	112	2	Q8K1F3_MOUSE	Q8k1f3 mus musculu
42	457	35.8	114	2	Q8K1F1_MOUSE	Q8k1f1 mus musculu
43	453.5	35.5	482	2	Q8K172_MOUSE	Q8k172 mus musculu
44	453	35.5	142	2	Q924Q1_MOUSE	Q924q1 mus musculu
45	453	35.5	237	2	Q569Y8_MOUSE	Q569y8 mus musculu

ALIGNMENTS

RESULT 1
Q7TQM2_MOUSE
ID Q7TQM2_MOUSE PRELIMINARY; PRT; 243 AA.
AC Q7TQM2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ScFv 6H8 protein (Fragment).
GN Name=scFv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/C;
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT "scFv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor.";
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAE00495.1; -; Genomic_DNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q7TQM2; 1-236.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1 1
SQ SEQUENCE 243 AA; 25976 MW; BEFFF64D2DCF4F76 CRC64;

Query Match 62.1%; Score 792.5; DB 2; Length 243;
Best Local Similarity 64.9%; Pred. No. 1.3e-53;
Matches 157; Conservative 30; Mismatches 48; Indels 7; Gaps 4;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              |||||||| || :|||||||||||||||:|| | |:|||| ||: ||||| | | :| ::|
Db          1 QVQLQQSGSELVRPGASVKLSCKASGYTFTTYWMHWVKQRHGQGLEWIGNIYPGSGITNY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              ::||: |  |||| ||||||| | || ||||||||:||||   ||| | || |||:|||||
Db         61 DEKFKNKGILTVDTSSSTAYMHLSSLASEDSAVYYCARG---GRGLDVWGAGTTLTVSSG 117

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-SYMHWYQQKSGTSPKR 180
              |||||||||||||||::||| :  | | |::||:|| ||  : : : ||||| | :|:
Db        118 GGGSGGGGSGGGGSDIQMTQSSSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPRL 177

Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQ-WSGYPLTFGAGTKLE 239
                |  : | :||| |||||||  |:|:|:|:: || ||||||| ||    ||| |||||
Db        178 LISGATSLETGVPSRFSGSGSGKDYTLSITSLQTEDVATYYCQQYWS--TRTFGGGTKLE 235

Qy        240 IK 241
              ||
Db        236 IK 237
```

```
Db        236 IK 237


RESULT 2
Q65ZC8_HUMAN
ID   Q65ZC8_HUMAN PRELIMINARY;      PRT;   244 AA.
AC   Q65ZC8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13057; CAA73500.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     244    244
SQ   SEQUENCE   244 AA;  26127 MW;  4B1F17868338F2BF CRC64;

  Query Match             61.4%;  Score 783.5;  DB 2;  Length 244;
  Best Local Similarity   61.3%;  Pred. No. 6.6e-53;
  Matches  149;  Conservative   39;  Mismatches   52;  Indels    3;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              |||| ||| |::||| |||:||||||||:|: : |:||:|: |: |||:| | | || : :
Db          1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSDHYMHWVRQAPGQGLEWMGWIDPNNGDTRF 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGR--GFDYWGQGTTVTVS 119
               |:|:|: |:| | | | |||::  | |:|:|||:||| |       | | ||||| ||||
Db         61 AQRFQGRVTMTRDTSISAAYMEVSRLRSDDTAVYYCAREGTGSAIYGMDVWGQGTLVTVS 120

Qy        120 SGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-SYMHWYQQKSGTSP 178
              || ||||||||||||||::||||: :||| |::||:|| ||  :  :: ||||| | :|
Db        121 SGGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQQKPGKAP 180

Qy        179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
              |  ||  | |||| | |||||||  ::|||||:: :| |||||||:| |||||| ||||
Db        181 KFLIYKASSLASGAPSRFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKL 240

Qy        239 EIK 241
              |||
Db        241 EIK 243


RESULT 3
Q65ZL2_9MURI
ID   Q65ZL2_9MURI PRELIMINARY;      PRT;   487 AA.
AC   Q65ZL2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   FV/M4.
GN   Name=M4-IFN-<tau>;
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=96272580; PubMed=8688499;
RA   Qi Y., Xiang J.;
RT   "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT   antibody secreted from myeloma cells.";
RL   Hum. Antibodies Hybridomas 6:161-166(1995).
DR   EMBL; S82493; AAB37424.2; -; mRNA.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   487 AA;  53578 MW;  C7BAB69F30555504 CRC64;

  Query Match             60.5%;  Score 771.5;  DB 2;  Length 487;
  Best Local Similarity   63.5%;  Pred. No. 1.3e-51;
  Matches  153;  Conservative   28;  Mismatches   53;  Indels    7;  Gaps    3;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||||||| || |||||||:|||||||:|| : ::| ||   : ||||| |:| |    |
Db         20 QVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWAKQKPEQGLEWIGYISPGNDDIKY 79

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              |:||:|||||| |||||||| | |||||||||||| |   |       :||||||:|  ||
Db         80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVYFCKRSYY-----GHWGQGTTLT-GSG 133

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-SYMHWYQQKSGTSPKR 180
              |||||||||||| |::||||| :| | || ||:|| || :: | : ||||| | ||:
Db        134 GGGSGGGGSGGGGSRIQMTQSPASLSVSVGELVTITCRASENIYSNLAWYQQKQGKSPQL 193

Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
               :|  : || ||| |||||||  ||| |:|:::||  :|||| : | | ||| ||:|||
Db        194 LVYAATNLADGVPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWGTPYTFGGGTRLEI 253

Qy        241 K 241
              |
Db        254 K 254


RESULT 4
Q6KB05_MOUSE
ID   Q6KB05_MOUSE PRELIMINARY;      PRT;   255 AA.
AC   Q6KB05;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ScFv B8E5 protein (Fragment).
GN   Name=scFv B8E5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Balb/c;
RA   Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA   Briand J.P., Hoebeke J.;
RT   "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT   monoclonal anti-M2 receptor antibody fragments.";
RL   J. Biol. Chem. 279:55697-55706(2004).
DR   EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR   HSSP; P01837; 1KCR.
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DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   255 AA;  27445 MW;  B68BD38395DF713B CRC64;

  Query Match             57.5%;  Score 733.5;  DB 2;  Length 255;
  Best Local Similarity   57.6%;  Pred. No. 5.3e-49;
  Matches  144;  Conservative   35;  Mismatches   60;  Indels   11;  Gaps    3;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||||||||  :| ||| |:|:|| |||::|: | |:||:|:  | |||:  ||     : |
Db          1 QVQLQQSGGDLVKPGGSLKVSCAASGFTFSSYGMSWVRQTPDKRLEWVATITSGGSYTYY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
                 :|: |:: | : :| |: : || |||:|:|:|||     |||  |||||||||:||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHINYRYDG-AFDYWGQGTTLTV 119

Qy        119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-------SYMHWYQ 171
              ||| |||||||||||||| : |||: :| | |||| |:| :| |:       :|: |||
Db        120 SSGGGGSGGGGSGGGGSDIVMAQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAWYQ 179

Qy        172 QKSGTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLT 231
              || | |||  ||  |   |||| ||:|||||  ::||||||:||| | ||||    ||||
Db        180 QKPGQSPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLT 239

Qy        232 FGAGTKLEIK 241
              ||||||||||
Db        240 FGAGTKLEIK 249


RESULT 5
Q921A6_MOUSE
ID   Q921A6_MOUSE PRELIMINARY;      PRT;   241 AA.
AC   Q921A6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-CEA 79 single chain Fv (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98170165; PubMed=9509426;
RA   Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA   Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT   "Cloning and characterization of cDNAs encoding VH and VL of a
RT   monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT   generation of a single-chain Fv molecule (scFv).";
RL   Mol. Cells 7:816-819(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA   Stark S.E., Caton A.J.;
RT   "Antibodies that are specific for a single amino acid interchange in a
RT   protein epitope use structurally distinct variable regions.";
RL   J. Exp. Med. 174:613-624(1991).
DR   EMBL; U88067; AAB48044.1; -; mRNA.
DR   PIR; S19965; S19965.
DR   PIR; S19967; S19967.
DR   PIR; S19968; S19968.
DR   PIR; S26325; S26325.
DR   HSSP; P01607; 1BWW.
DR   Ensembl; ENSMUSG00000021155; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     241    241
SQ   SEQUENCE   241 AA;  26086 MW;  0276887248E9C771 CRC64;

  Query Match             56.9%;  Score 726.5;  DB 2;  Length 241;
  Best Local Similarity   58.8%;  Pred. No. 1.8e-48;
  Matches  144;  Conservative   34;  Mismatches   56;  Indels   11;  Gaps    5;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:|||||||:||| :||:|||||||:|| | ||||||: || |:|:| |  | |  :|
Db          1 QVKLQQSGPELKKPGETVKISCKASGYTFTDYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
                 |:|:   ::: |:||||: : :| :||:| |||||     | ||||||||||||||
Db         61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARKDL-LRYFDYWGQGTTVTVSSG 119

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVS-YMHWYQQKSGTSPKR 180
              |||||||||||||||||||||: :||| | |||:|| ||  :: |: ||| | |  |:
Db        120 GGGSGGGGSGGGGSDIELTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRS 179

Qy        181 ----WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGT 236
                  ||    :  |:| |||||||  || :||::| || |||||  :     ||| ||
Db        180 AHTLHIY----IQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLHYDNLH-TFGGGT 234

Qy        237 KLEIK 241
              |||:|
Db        235 KLELK 239


RESULT 6
Q65ZC9_HUMAN
ID   Q65ZC9_HUMAN PRELIMINARY;      PRT;   240 AA.
AC   Q65ZC9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C1q/7;
RX   MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13056; CAA73499.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     240    240
SQ   SEQUENCE   240 AA;  25569 MW;  FDCFD3645F64B373 CRC64;

  Query Match             56.3%;  Score 718.5;  DB 2;  Length 240;
  Best Local Similarity   57.4%;  Pred. No. 7.3e-48;
  Matches  139;  Conservative   43;  Mismatches   55;  Indels    5;  Gaps    4;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASS- 60
              |||| |||  | :|| |::||| |||::|: | |:||:|: || |||: :|: |:|::
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIS-YDGSNKY 59

Qy         61 YNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              |    :|: |:: | | :| |: : || :||:|||:|||    |   | ||:|| |||||
Db         60 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDW--GDSLDPWGKGTLVTVSS 117
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Qy        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-SYMHWYQQKSGTSPK 179
              | |||||||||||||||::||||: :||| |::||:|| ||  :  :: ||||| | :||
Db        118 GGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYRWLAWYQQKPGKAPK 177

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
                ||  | |||  | ||||||||  ::|||||:: :| |||||||:| ||||||  |||||
Db        178 LLIYKASSLASRAPSRFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLE 237

Qy        240 IK 241
              ||
Db        238 IK 239
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RESULT 7
Q65ZQ7_9MURI
ID Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE B3(Fv)-PE40 (Fragment).
GN Name=B3(Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB19971.2; -; mRNA.
DR SMR; Q65ZQ7; 4-247.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 248 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

  Query Match 50.5%; Score 645; DB 2; Length 248;
  Best Local Similarity 51.0%; Pred. No. 3.9e-42;
  Matches 126; Conservative 41; Mismatches 74; Indels 6; Gaps 1;

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Qy          1 MQVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASS 60
              | |:| :||  | :|| |:|||| ||::|: | | ||:|:  | |||:  |:  : :::
Db          1 MDVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQTPEKRLEWVAYISNDDSSAA 60

Qy         61 YNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              |:   :|: |:: | : :| |: :  | |||:|:| ||||   |  | |||||| |||||
Db         61 YSDTVKGRFTISRDNARNTLYLQMSRLKSEDTAIYSCARGLAWGAWFAYWGQGTLVTVSS 120

Qy        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV------SYMHWYQQKS 174
              | |||||||||||||: :||||  :  | |:: :::| :|  :      :|: || ||
Db        121 GGGGSGGGGSGGGGSDVLMTQSPLSLPVSLGDQASISCRSSQIIVHSNGNTYLEWYLQKP 180

Qy        175 GTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGA 234
              | |||  ||  |   |||| |||||||  ::| || |||||   |||| | |  | |||:
Db        181 GQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGS 240

Qy        235 GTKLEIK 241
              |||||||
Db        241 GTKLEIK 247
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RESULT 8
Q925S1_MOUSE
ID Q925S1_MOUSE PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
RA Yan X.J., Hou Y., Su C.Z.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after gamma-irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -; mRNA.
DR HSSP; P01665; 1QNZ.
DR Ensembl; ENSMUSG00000058040; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

  Query Match 49.2%; Score 628; DB 2; Length 218;
  Best Local Similarity 55.8%; Pred. No. 7e-41;
  Matches 121; Conservative 35; Mismatches 55; Indels 6; Gaps 2;

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Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:|||||||:||| :|::|||||||:||   | ||::  || |:||| |  ::|   |
Db          3 QVKLQQSGPELKKPGETVRISCKASGYTFTTAGMQWVQKMPGKGLKWIGWINTHSGVPKY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
                ::|:|:   ::: |:||||: : :| :||:| ||| |  ||| || ||||||||||||
Db         63 AEEFKGRFAFSLETSASTAYLQISNLKNEDTATYFCMRWDYDG-GFAYWGQGTTVTVSSG 121

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-----SYMHWYQQKSGT 176
              |||||||||| ||||| |||||| :: | |:: |::| || ||     |:|:|:||| |
Db        122 GGGSGGGGSGSGGSDIVLTQSPASLAVSLGQRATISCRASESVDNIGISFMNWFQQKPGQ 181

Qy        177 SPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVE 213
              ||  ||  ||  ||||     ||||  :|| |  :|
Db        182 PPKLLIYAASKQGSGVPAGLLASGSGTDFSLNIYPME 218
```

RESULT 9
Q925S2_MOUSE
ID Q925S2_MOUSE PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RX   PubMed=11819679;
RA   Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
RA   Yan X.J., Hou Y., Su C.Z.;
RT   "Mechanism of exogenous nucleic acids and their precursors improving
RT   the repair of intestinal epithelium after gamma-irradiation in mice.";
RL   World J. Gastroenterol. 6:709-717(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RA   Cui D., Zeng G., Yan X., Li X., Su C.;
RT   "Cloning of mouse genes related to repairing of intestinal epithelium
RT   of the irradiated mice by treatment with the intestinal RNA of mice of
RT   the same strain.";
RL   Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR   EMBL; AF240167; AAK43732.1; -; mRNA.
DR   HSSP; P01751; 1A6W.
DR   SMR; Q925S2; 3-124.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   170 AA;  17978 MW;  5042823CC6C10F38 CRC64;

  Query Match             42.6%;  Score 543;  DB 2;  Length 170;
  Best Local Similarity   66.4%;  Pred. No. 2.1e-34;
  Matches  101;  Conservative   23;  Mismatches   16;  Indels   12;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:|||||||: :|| |||:||| |||:|| |:|:|:| :| :|||||:|: |:| ::|
Db          3 QVKLQQSGPEVVRPGVSVKISCKGSGYTFTDYSMHWLKMNHAQSLEWIGIISTYDGNTNY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGR--GFDYWGQGTTVTVS 119
              ||||:||||:|||||| ||||:|  |||:|||:|:|||| | |    ||||||||||||
Db         63 NQKFKGKATMTVDKSSITAYMELARLTSDDSAIYYCARGAYYGSFYYFDYWGQGTTVTVS 122

Qy        120 SGVGGSGGGGSGGGGSDIELTQSPAIMSASPG 151
              || ||||||||||||:          |:|||
Db        123 SGGGGSGGGGSGGGGSE----------SSSPG 144


RESULT 10
Q7TMK1_MOUSE
ID   Q7TMK1_MOUSE PRELIMINARY;      PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein AI324046.
GN   Name=AI324046;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -; mRNA.
DR   HSSP; P01865; 1KB5.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   470 AA;  51728 MW;  6D90E4DF896BB090 CRC64;

  Query Match             40.3%;  Score 514.5;  DB 2;  Length 470;
  Best Local Similarity   52.1%;  Pred. No. 1.1e-31;
  Matches  122;  Conservative   19;  Mismatches   46;  Indels   47;  Gaps    8;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|||||||||| |||||||:|||||||:|||| |:|||||||||||||||: | || :||
Db         20 EVQLQQSGPELVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSY 79

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGR--GFDYWGQGTTVTVS 119
              ||||:|||||||||||||:| |||||||||:|||  | |    || || |||||||
Db         80 NQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYCARYYYSGSYWYFDVWGAGTTVTVS 139

Qy        120 SGVGGSGGGGSGGGGSDIELTQSPAIMSASP------GEKVTMTCSASSSVSYMHWYQQK 173
              |                       | :|::    |      |  ||: |
Db        140 SAT-----------------TTAPSVYPLVPGCGDTSGSSVTLGCLV------------ 169

Qy        174 SGTSPK----RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQ 223
              |  |:    :| |    |:|||    |   ||  |||  ||:     :|:  |
Db        170 KGYFPEPVTVKWNY--GALSSGVRTVSSVLQSG-FYSL--SSLVTVPSSTWPSQ 218


RESULT 11
Q6PJA7_MOUSE
ID   Q6PJA7_MOUSE PRELIMINARY;      PRT;   472 AA.
AC   Q6PJA7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   Name=Igh-1a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018535; AAH18535.1; -; mRNA.
DR   HSSP; P01865; 1KB5.
DR   MGI; MGI:96443; Igh-1a.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  52299 MW;  165169C23D55D4AB CRC64;

  Query Match             39.4%;  Score 502.5;  DB 2;  Length 472;
  Best Local Similarity   46.1%;  Pred. No. 9.8e-31;
  Matches  118;  Conservative   26;  Mismatches   59;  Indels   53;  Gaps    9;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|||||||||| | |||||:|||||||:|: | |:|||||||||||||| | | || : |
Db         20 EVQLQQSGPELVKTGASVKMSCKASGYTFSDYYMHWVKQSHGKSLEWIGYIYPNNGGNGY 79

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG-----GYDGRGFDYWGQGTTV 116
              ||||:|||||||||||||:| ||||||||||:||||       ||    |||||||||:
Db         80 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARGYISYYSYD-HYFDYWGQGTTI 138

Qy        117 TVSSGVGGSGGGGSGGGGSDIELTQSPAIMSASP------GEKVTMTCSASSSVSYMHWY 170
              ||||                    | :|::   :|      |  ||: |      |
Db        139 TVSSA----------------KTTAPSVYPLAPVCGDTTGSSVTLGCLVK---GYF--- 175

Qy        171 QQKSGTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPL 230
                  |    :::  |:|||   |      : |:|: |          |     |    :
Db        176 -----PEPVTLTWNSGSLSSGV-HTFPAVLQSDLYTLSSS-------VTVTSSTWPSQSI 222

Qy        231 TF-----GAGTKLEIK 241
              |       : ||:: |
Db        223 TCNVAHPASSTKVDKK 238


RESULT 12
Q4VAB6_MOUSE
ID   Q4VAB6_MOUSE PRELIMINARY;      PRT;   483 AA.
AC   Q4VAB6;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC096462; AAH96462.1; -; mRNA.
KW   Hypothetical protein.
SQ   SEQUENCE   483 AA;  52436 MW;  368E7BEE6B6DE9EF CRC64;

  Query Match             38.9%;  Score 497;  DB 2;  Length 483;
  Best Local Similarity   48.5%;  Pred. No. 2.7e-30;
  Matches  114;  Conservative   25;  Mismatches   50;  Indels   46;  Gaps    7;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ::|| |||||| ||| |||:|||||||:|| | |:||:|||||||||||| | | :||:||
Db         20 EIQLHQSGPELVKPGTSVKMSCKASGYTFTNYYMHWVRQSHGKSLEWIGYIYPNSGATSY 79

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              ||||:||||||||||:||||:| ||||:|||||:||||      |||||||||:||||
Db         80 NQKFKGKATLTVDKSSTTAYMELRSLTSDDSAVYYCARGDLRTGLFDYWGQGTTLTVSS- 138

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIM-----SASPGEKVTMTCSASSSVSYMHWYQQKSGT 176
                          |  : | |       |   : | : |         :| |   |||
Db        139 ---------------EPAREPTIYPLTFPQALSSDPVIIGC-------LIHDY-FPSGT 174

Qy        177 SPKRW---------IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYC 222
                  |         :     ||||  ||:: |       ||: :||  :  :  |
Db        175 MNVTWGKSGKDITTVNFPPALASG--GRYTMSS-----QLTLPAVECPEGESVKC 222


RESULT 13
Q8K1F0_MOUSE
ID   Q8K1F0_MOUSE PRELIMINARY;      PRT;   112 AA.
AC   Q8K1F0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-VIPase light chain variable region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA   Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2499887;
RA   Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT   "Two murine natural polyreactive autoantibodies are encoded by
RT   nonmutated germ-line genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR   EMBL; AF516285; AAM64203.1; -; Genomic_DNA.
DR   PIR; A33933; A33933.
DR   PIR; PC4405; PC4405.
DR   HSSP; P01837; 1ORQ.
DR   SMR; Q8K1F0; 3-112.
DR   Ensembl; ENSMUSG00000062047; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11901 MW;  F6644663201AA239 CRC64;

  Query Match             38.9%;  Score 496;  DB 2;  Length 112;
  Best Local Similarity   92.2%;  Pred. No. 5.7e-31;
  Matches   95;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        139 LTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRFSG 198
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          4 LTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARFSG 63

Qy        199 SGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              |||||||||||| | || |||||||||  | ||| |||||||
Db         64 SGSGNSYSLTISSTEGEDAATYYCQQWSSNPPTFGGGTKLEIK 106


RESULT 14
Q58EV6_MOUSE
ID   Q58EV6_MOUSE PRELIMINARY;      PRT;   235 AA.
AC   Q58EV6;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Igk-C protein.
GN   Name=Igk-C;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC091738; AAH91738.1; -; mRNA.
DR   SMR; Q58EV6; 23-235.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   235 AA;  25719 MW;  BE4E4ABDD2578252 CRC64;

  Query Match             38.9%;  Score 496;  DB 2;  Length 235;
  Best Local Similarity   89.5%;  Pred. No. 1.4e-30;
  Matches   94;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        137 IELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRF 196
              | |||||||||||||||||||||||| |||||||||||||||||||||||||||||| ||
Db         24 IVLTQSPAIMSASPGEKVTMTCSASSGVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 83

Qy        197 SGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              ||||| ||||||||:|||| ||||||||:  ||||||||||::|
Db         84 SGSGSGTSYSLTISSMEAEDAATYYCQQWTSNPLTFGAGTKLDLK 128


RESULT 15
Q91WR1_MOUSE
ID   Q91WR1_MOUSE PRELIMINARY;      PRT;   488 AA.
AC   Q91WR1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Igh-VJ558 protein.
GN   Name=Igh-VJ558;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013539; AAH13539.1; -; mRNA.
DR   HSSP; P01751; 1A6W.
DR   Ensembl; ENSMUSG00000021155; Mus musculus.
DR   MGI; MGI:96486; Igh-VJ558.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   488 AA;  52965 MW;  F12068460B400B9D CRC64;

  Query Match             38.8%;  Score 495.5;  DB 2;  Length 488;
  Best Local Similarity   49.6%;  Pred. No. 3.6e-30;
  Matches  120;  Conservative   20;  Mismatches   47;  Indels   55;  Gaps   10;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|||||||||| |||||||||||||||: | | :|||||||||||||| | |||| :||
Db         20 EVQLQQSGPELVKPGASVKLSCKASGYTITDYYVNWVKQSHGKSLEWIGDINPYNGGTSY 79

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG-------GYDGRGFDYWGQGT 114
              ||||:|||||||||||| ||| | :|||:|||||:||||        || || |||||||
Db         80 NQKFKGKATLTVDKSSSIAYMQLNNLTSDDSAVYYCARGPVYYSYFSYD-RG-DYWGQGT 137

Qy        115 TVTVSSGVGGSGGGGSGGGGSDIELTQSPAIM-----SASPGEKVTMTCSASSSVSYMHW 169
               ||||:                  |  : | |       |   : | : |         :|
Db        138 LVTVSA-----------------EPAREPTIYPLTFPQALSSDPVIIGC-------LIHD 173

Qy        170 YQQKSGTSPKRW---------IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATY 220
              |   |||    |         :     ||||  ||:: |       ||: :||  :  :
Db        174 Y-FPSGTMNVTWGKSGKDITTVNFPPALASG--GRYTMSS-----QLTLPAVECPEGESV 225

Qy        221 YC 222
               |
Db        226 KC 227


Search completed: April  3, 2006, 05:31:28
Job time : 58 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 3, 2006, 05:29:59 ; Search time 323 Seconds
(without alignments)
327.834 Million cell updates/sec

Title: US-09-979-539-1
Perfect score: 1276
Sequence: 1 MQVQLQQSGPELEKPGASVK.....CQQWSGYPLTFGAGTKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1276	100.0	241	2	ABB76197	Abb76197 Anti-meso
2	1276	100.0	241	4	AAB50019	Aab50019 Antimesot
3	1025.5	80.4	242	6	ABR62132	Abr62132 Single ch
4	1025.5	80.4	242	8	ADT91209	Adt91209 Single ch
5	1010.5	79.2	239	4	AAB47111	Aab47111 scFv 508F
6	1010.5	79.2	239	6	AAO16066	Aao16066 Human neu
7	1010.5	79.2	239	8	ADJ88113	Adj88113 Human bet
8	1004	78.7	494	9	ADV66089	Adv66089 Anti-CD3-
9	1004	78.7	500	9	ADV66137	Adv66137 Anti-CD3-
10	1004	78.7	500	9	ADV66095	Adv66095 Anti-CD3-
11	1004	78.7	500	9	ADV66097	Adv66097 Anti-CD3-
12	1004	78.7	503	9	ADV66131	Adv66131 Anti-CD3-
13	1004	78.7	503	9	ADV66093	Adv66093 Anti-CD3-
14	1004	78.7	503	9	ADV66091	Adv66091 Anti-CD3-
15	1004	78.7	503	9	ADV14540	Adv14540 Bispecifi
16	1004	78.7	503	9	AEA52450	Aea52450 Human CD3
17	1004	78.7	504	9	ADV14536	Adv14536 Bispecifi
18	1004	78.7	504	9	AEA52449	Aea52449 Human CD3
19	1003	78.6	261	8	ADT91213	Adt91213 Single ch
20	1002.5	78.6	498	8	ADW38798	Adw38798 Single ch
21	998.5	78.3	239	7	ADC79232	Adc79232 Control s
22	997.5	78.2	239	7	ADC79231	Adc79231 Anti-CA12
23	995	78.0	242	2	AAR79872	Aar79872 Anti-EGFR
24	993	77.8	244	2	AAR79867	Aar79867 Anti-EGFR
25	989.5	77.5	242	6	ABR62131	Abr62131 Single ch
26	989.5	77.5	242	8	ADT91207	Adt91207 Single ch
27	987	77.4	242	2	AAR79870	Aar79870 Anti-EGFR
28	985	77.2	244	2	AAR79873	Aar79873 Anti-EGFR
29	982.5	77.0	297	2	AAY05363	Aay05363 HBV speci
30	981.5	76.9	599	2	AAW37132	Aaw37132 Anti-Tac(
31	981.5	76.9	599	3	AAY87477	Aay87477 Anti-Tac(
32	979.5	76.8	309	4	AAB70841	Aab70841 SNV-env l
33	979	76.7	244	2	AAR79868	Aar79868 Anti-EGFR
34	977	76.6	242	2	AAR79871	Aar79871 Anti-EGFR
35	976.5	76.5	239	3	AAB12563	Aab12563 Anti-TAC
36	976.5	76.5	239	4	AAB36826	Aab36826 Anti-TAC
37	976.5	76.5	599	2	AAW95462	Aaw95462 Anti-Tac(
38	972.5	76.2	330	4	AAB70842	Aab70842 SNV-env l
39	972	76.2	246	2	AAR79869	Aar79869 Anti-EGFR
40	967.5	75.8	492	8	ADQ91082	Adq91082 Antibody
41	967.5	75.8	492	8	ADQ91098	Adq91098 Antibody
42	967.5	75.8	492	8	ADQ91102	Adq91102 Antibody
43	967.5	75.8	497	9	ADV66125	Adv66125 Anti-CD3-
44	967.5	75.8	503	9	ADV66087	Adv66087 Anti-CD3-
45	967.5	75.8	503	9	ADV66135	Adv66135 Anti-CD3-

ALIGNMENTS

RESULT 1
ABB76197
ID ABB76197 standard; protein; 241 AA.
XX
AC ABB76197;
XX
DT 05-AUG-2002 (first entry)
XX
DE Anti-mesothelin scFv SS.
XX
KW Mesothelin; antibody; scFv; mouse; mesothelioma; ovarian cancer;
KW stomach cancer; squamous cell cancer; antitumour; therapy; diagnosis;
KW immunotoxin.
XX
OS Mus sp.
XX

FH	Key	Location/Qualifiers
FT	Region	1. .31
FT		/note= "heavy chain framework region 1"
FT	Region	32. .36
FT		/note= "heavy chain complementarity determining region 1"
FT	Region	37. .50
FT		/note= "heavy chain framework region 2"
FT	Region	51. .67
FT		/note= "heavy chain complementarity determining region 2"
FT	Region	68. .99
FT		/note= "heavy chain framework region 3"
FT	Region	100. .109
FT		/note= "heavy chain complementarity determining region 3"
FT	Region	110. .120
FT		/note= "heavy chain framework region 4"
FT	Region	121. .135
FT		/note= "linker"
FT	Region	136. .158
FT		/note= "light chain framework region 1"
FT	Region	159. .168
FT		/note= "light chain complementarity determining region 1"
FT	Region	169. .183
FT		/note= "light chain framework region 2"
FT	Region	184. .190
FT		/note= "light chain complementarity determining region 2"
FT	Region	191. .222
FT		/note= "light chain framework region 3"
FT	Region	223. .231
FT		/note= "light chain complementarity determining region 3"
FT	Region	232. .241
FT		/note= "light chain framework region 4"

XX
PN WO9928471-A2.
XX
PD 10-JUN-1999.
XX
PF 25-NOV-1998; 98WO-US025270.
XX
PR 01-DEC-1997; 97US-0067175P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Pastan IH, Chowdhury PS;
XX
DR WPI; 1999-371123/31.
DR N-PSDB; ABL57231.
XX
PT New anti-mesothelin antibodies.
XX
PS Claim 2; Fig 1; 63pp; English.
XX
CC The present sequence is the protein sequence of anti-mesothelin scFv
CC antibody SS. This single-chain antibody was produced by immunising a
CC mouse with cDNA encoding mesothelin, creating a phage library from mRNA
CC isolated from the spleen of the immunised animal, and enrichment of anti-
CC mesothelin phage over 3 rounds of panning. scFv SS is composed of a heavy
CC chain variable region (VH) joined to a light chain variable region (VL)
CC via a peptide linker. According to Kabat's classification, the VH belongs
CC to sub-group IIA and family V and the VL belongs to sub-group VI and
CC family XI. A claimed anti-mesothelin antibody binds recombinant
CC mesothelin with a dissociation constant of less than 3 x 10 power -8 M
CC and specifically binds to cells expressing mesothelin on their cell
CC surface. The antibody comprises SS scFv, the VH and VL region of SS scFv
CC or the complementarity determining regions of SS scFv. It is preferably
CC conjugated to a therapeutic agent, particularly Pseudomonas exotoxin or
CC its cytotoxic fragment. The resulting immunoconjugate is used in a
CC claimed method for inhibiting the growth of a malignant cell that
CC expresses mesothelin on its cell surface, especially in mesothelioma,
CC ovarian cancer, stomach cancer or squamous cell cancer. The antibody can
CC also be used to detect mesothelin in a biological sample
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 1276; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.8e-77;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MQVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASS 60

Qy         61 YNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120

Qy        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKR 180

Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240

Qy        241 K 241
              |
Db        241 K 241
```

RESULT 2
AAB50019
ID AAB50019 standard; protein; 241 AA.
XX
AC AAB50019;
XX

DT 14-MAR-2001 (first entry)
XX
DE Antimesothelin antibody SS single-chain Fv protein.
XX
KW Mesothelin; SS antibody; single-chain Fv; scFv; cytostatic;
KW cancer therapy; ovarian cancer; mesothelioma.
XX
OS Unidentified.
XX
PN WO200073346-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014829.
XX
PR 27-MAY-1999; 99US-0160071P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Pastan I, Chowdhury PS;
XX
DR WPI; 2001-061517/07.
XX
PT Novel polypeptides comprising mutated antimesothelin antibody heavy or
PT light chain variable region, having greater binding affinity for the
PT antigen, useful as diagnostic and therapeutic agents for ovarian cancers.
XX
PS Disclosure; Fig 1; 70pp; English.
XX
CC The present sequence is antimesothelin antibody SS single chain Fv
CC protein. This sequence was used to generate mutant antibody heavy or
CC light chain variable regions, which have 5 times higher binding affinity
CC for mesothelin antigen than the parental antibody (the present sequence).
CC The mutant proteins of the present invention have substition(s) in the
CC complementarity determining region (CDR). Malignant cells express
CC mesothelin on their surfaces, and so the mutant proteins of the present
CC invention can be used to target immunotoxin to cells expressing
CC mesothelin on their surface i.e. malignant cells. The mutant proteins of
CC the present invention can therefore be used to treat ovarian cancers,
CC mesotheliomas, and several other types of human cancers in which the
CC cells bear the mesothelin antigen
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 1276; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.8e-77;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MQVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASS 60

Qy         61 YNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120

Qy        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKR 180

Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240

Qy        241 K 241
              |
Db        241 K 241
```

RESULT 3
ABR62132
ID ABR62132 standard; protein; 242 AA.
XX

```
AC   ABR62132;
XX
DT   29-AUG-2003  (first entry)
XX
DE   Single chain antibody sequence #SEQ ID 20.
XX
KW   Tumour; drug delivery; ligand; cancer; carcinoma; bladder; breast;
KW   cervix; colorectum; lung; ovary; pancreas; prostate; stomach;
KW   cholangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma;
KW   multiple myeloma; osteosarcoma; head; neck; radiation; x-ray; antibody.
XX
OS   Synthetic.
XX
PN   WO2003028640-A2.
XX
PD   10-APR-2003.
XX
PF   27-SEP-2002; 2002WO-US030917.
XX
PR   03-OCT-2001; 2001US-0328123P.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   Hallahan DE,  Qu S;
XX
DR   WPI; 2003-421186/39.
XX
PT   Identifying molecule that binds to irradiated tumor in a subject, by
PT   exposing tumor to ionizing radiation, administering library of diverse
PT   molecules and isolating library molecules from tumor to identify the
PT   target.
XX
PS   Claim 38; Page 107-108; 108pp; English.
XX
CC   The invention relates to a method for identifying a molecule that binds
CC   an irradiated tumour in a subject. The method of the invention involves
CC   exposing a tumour to ionizing radiation, administering a library of
CC   diverse molecules to a subject, and isolating one or more molecules of
CC   the library from the tumour. The method of the invention is useful for
CC   identifying a molecule that binds an irradiated tumour in a subject e.g.
CC   warm-blooded vertebrate and human, and also for tumour detection. The
CC   tumour is a primary or a metastasized tumour such as carcinoma of the
CC   bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate,
CC   stomach, cholangiocarcinoma, gastric sarcoma, glioma, lymphoma, melanoma,
CC   multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The
CC   method of the invention is useful for X-ray-guided delivery of a
CC   therapeutic composition, a diagnostic composition or their combinations
CC   to a tumour in a subject. The current sequence represents a single chain
CC   antibody sequence that was identified following in vivo panning to
CC   irradiated tumours. This antibody binds platelet membrane glycoprotein
CC   IIB
XX
SQ   Sequence 242 AA;

  Query Match             80.4%;  Score 1025.5;  DB 6;  Length 242;
  Best Local Similarity   81.7%;  Pred. No. 9.7e-61;
  Matches  196;  Conservative   13;  Mismatches   30;  Indels    1;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:|||||||| |||||||:|||||||:|| | |:|||| |: ||||| | |||  : |
Db          3 QVKLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              |:||:||| || |||||||||:| |||||||||:||| |  |   ||||||||||||||
Db         63 NEKFKGKAALTSDKSSSTAYMELSSLTSEDSAVYYCARFGNYG-ALDYWGQGTTVTVSSG 121

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              |||||||||||||||||||| ||||||||||:|||||||||||:||| ||||| |
Db        122 GGGSGGGGSGGGGSDIELTQSPTIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKPW 181

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              || || |||||| |||||||| ||||||||:|||| ||||||||| |||||| |||||||
Db        182 IYGTSNLASGVPVRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSYPLTFGGGTKLEIK 241
```

```
RESULT 4
ADT91209
ID   ADT91209 standard; protein; 242 AA.
XX
AC   ADT91209;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Single chain variable fragment (scFv) antibody #2.
XX
KW   Tumour; benign intracranial meningioma; arteriovenous malformation;
KW   angioma; macular degeneration; melanoma; adenocarcinoma;
KW   malignant glioma; prostatic carcinoma; kidney carcinoma;
KW   bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
KW   lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
KW   liver carcinoma; breast carcinoma; ovary carcinoma; angiofibroma;
KW   retrolental fibroplasia; haemangioma; Kaposi's sarcoma;
KW   single chain variable fragment; scFv; antibody.
XX
OS   Unidentified.
XX
PN   US2004191249-A1.
XX
PD   30-SEP-2004.
XX
PF   20-OCT-2003; 2003US-00689006.
XX
PR   28-APR-2000; 2000WO-US011485.
PR   09-NOV-2001; 2001US-00914605.
PR   27-SEP-2002; 2002US-00259087.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   Hallahan DE,  Mernaugh R;
XX
DR   WPI; 2004-698661/68.
DR   N-PSDB; ADT91208.
XX
PT   Screening phage-displayed antibodies binding to radiation-inducible
PT   neoantigen on cell, comprises contacting cell with antibodies, treating
PT   cell with radiation, contacting cell with antibodies not binding to cell,
PT   detecting bound antibody.
XX
PS   Claim 4; SEQ ID NO 20; 64pp; English.
XX
CC   The invention relates to a method for screening phage-displayed
CC   antibodies binding to radiation-inducible neoantigen on cell. The method
CC   involves contacting cell with antibodies, treating cell with radiation,
CC   contacting cell with antibodies not binding to cell and detecting the
CC   bound antibody. The method is useful for screening several phage-
CC   displayed antibodies for an ability to bind to a radiation-inducible
CC   neoantigen present on a cell, where the cell is tumour cell chosen from
CC   benign intracranial meningiomas, arteriovenous malformation, angioma,
CC   macular degeneration, melanoma, adenocarcinoma, malignant glioma,
CC   prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
CC   carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
CC   carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
CC   carcinoma, solid tumours, solid tumour metastases, angiofibromas,
CC   retrolental fibroplasias, haemangiomas, Kaposi's sarcoma, head and neck
CC   carcinomas and their combinations or vascular endothelial cell. The
CC   present sequence is a single chain variable fragment (scFv) antibody that
CC   binds to radiation-inducible neoantigens.
XX
SQ   Sequence 242 AA;

  Query Match             80.4%;  Score 1025.5;  DB 8;  Length 242;
  Best Local Similarity   81.7%;  Pred. No. 9.7e-61;
  Matches  196;  Conservative   13;  Mismatches   30;  Indels    1;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:|||||||| |||||||:|||||||:|| | |:|||| |: ||||| | |||  : |
```

```
Db          3 QVKLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              |:||:||| || |||||||||:| ||||||||||:||| |   |   ||||||||||||||
Db         63 NEKFKGKAALTSDKSSSTAYMELSSLTSEDSAVYYCARFGNYG-ALDYWGQGTTVTVSSG 121

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              |||||||||||||||||||| ||||||||||:||||||||||||:||| ||||| |
Db        122 GGGSGGGGSGGGGSDIELTQSPTIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKPW 181

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              || || |||||| |||||||| ||||||||:|||| |||||||| |||||| |||||||
Db        182 IYGTSNLASGVPVRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSYPLTFGGGTKLEIK 241
```

RESULT 5
AAB47111
ID AAB47111 standard; protein; 239 AA.
XX
AC AAB47111;
XX
DT 04-JUN-2001 (first entry)
XX
DE scFv 508F.
XX
KW Human; prion protein; plaque forming disease; display vehicle; kuru;
KW aggregating protein; amyloid plaque; brain; early onset; senility;
KW Alzheimer's disease; late onset; pre-symptomatic; SAA amyloidosis;
KW hereditary Icelandic syndrome; multiple myeloma; scrapie; BSE; CJD;
KW bovine spongiform encephalopathy; Creutzfeldt-Jakob Disease; FFI;
KW Gerstmann-Streussler-Sheinker Disease; GSS; fatal familial insomnia;
KW antibody.
XX
OS Synthetic.
XX

Key	Location/Qualifiers
FT Domain	1. .120
FT	/note= "Heavy chain"
FT Region	31. .35
FT	/label= CDR1
FT Region	50. .66
FT	/label= CDR2
FT Region	99. .107
FT	/label= CDR3
FT Peptide	121. .133
FT	/note= "Linker"
FT Domain	134. .239
FT	/note= "Light chain"
FT Region	157. .166
FT	/label= CDR1
FT Region	182. .188
FT	/label= CDR2
FT Region	221. .229
FT	/label= CDR3

XX
PN WO200118169-A2.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-IL000518.
XX
PR 03-SEP-1999; 99US-0152417P.
PR 29-DEC-1999; 99US-00473653.
PR 31-JUL-2000; 2000US-00629971.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
PI Solomon B, Frenkel D, Hanan E;
XX
DR WPI; 2001-244564/25.
DR N-PSDB; AAC85539.
XX
PT Treating amyloidgenic disease such as Alzheimer's disease, BSE or CJD
PT comprises presentation of plaque derived antigens or epitopes on a
PT display vehicle, and introducing the vehicle into the recipient.
XX
PS Example 2; Fig 11; 120pp; English.
XX
CC This sequence shows scFv 508F heavy chain, linker and light chain. The
CC scFv fragment was derived from the 508 IgM hybridoma which is generated
CC from splenocytes of a mouse that has been immunised with a peptide
CC corresponding to the 16 amino terminal residues of beta-AP conjugated to
CC keyhole limpet hemocyanin used a carrier. The resultant variable chain
CC fragments may be used in the method of the invention. Cys 96 of the VL
CC fragment was replaced with various amino acids to see if production yield
CC or stability were effected without having an adverse effect on its
CC binding affinity. The invention provides an agent for treating a plaque
CC forming disease. Antigenic polypeptides are displayed on a display
CC vehicle and are capable of eliciting antibodies capable of disaggregating
CC the aggregating protein and/or of preventing aggregation of the
CC aggregating protein. This reduces formation of amyloid plaques in the
CC brain of victims of plaque forming diseases, e.g. early onset Alzheimer's
CC disease, late onset Alzheimer's disease, pre-symptomatic Alzheimer's
CC disease, SAA amyloidosis, hereditary Icelandic syndrome, senility,
CC multiple myeloma, scrapie, bovine spongiform encephalopathy (BSE), kuru,
CC Creutzfeldt-Jakob Disease (CJD), Gerstmann-Streussler- Sheinker Disease
CC (GSS) and fatal familial insomnia (FFI)
XX
SQ Sequence 239 AA;

Query Match 79.2%; Score 1010.5; DB 4; Length 239;
Best Local Similarity 79.8%; Pred. No. 9.6e-60;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|| || :|| |||:||| |||:|| | |:|||||| ||||||||:|: | | :||
Db          1 QVKLQESGAELVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
              ||||:||||:|||||||||||:|  |||||||:|:||||    |    |||||| |||||
Db         61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy        119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
              ||| ||||| ||||||||||||||||||||||||||||||||:|||||||||| ||||
Db        117 SSGGGGSGGVGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSP 176

Qy        179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
              |||||||||||||| ||||||| ||||||||:|||| ||||| | | || ||| | ||
Db        177 KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPFTFGGGAKL 236

Qy        239 EIK 241
              |||
Db        237 EIK 239
```

RESULT 6
AAO16066
ID AAO16066 standard; protein; 239 AA.
XX
AC AAO16066;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human neurological/CNS disease treatment method-related protein.
XX
KW Vaccine; gene therapy; neurological disease; CNS disorder;
KW central nervous system disorder; olfactory system; Alzheimer's disease;
KW Creutzfeld-Jakob disease; Huntington's chorea; Parkinson's disease;
KW viral infection of the brain; brain tumour; lysosomal storage disease;
KW multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO200274243-A2.
XX
PD 26-SEP-2002.

XX
PF 15-MAR-2002; 2002WO-US008042.
XX
PR 15-MAR-2001; 2001US-00808037.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (MCIN/) MCINNIS P.
XX
PI Solomon B, Frenkel D;
XX
DR WPI; 2003-040542/03.
DR N-PSDB; AAL51099.
XX
PT Treating or diagnosing neurological diseases of the central nervous
PT system, e.g. Alzheimer's disease, comprises displaying a polypeptide or
PT diagnostic agent on viral display vehicle and introducing or detecting
PT the display vehicle.
XX
PS Example 2; Fig 11A; 214pp; English.
XX
CC The invention comprises a method for treating a neurological disease or a
CC central nervous system (CNS) disorder. The method involves displaying a
CC therapeutic molecule capable of treating the neurological disease or CNS
CC disorder on a viral display vehicle. The viral display vehicle is then
CC introduced into the olfactory system of a subject to treat the disease or
CC disorder. The method of the invention is useful for preventing, treating
CC and diagnosing neurological diseases or CNS disorders, such as:
CC Alzheimer's disease; Creutzfeld-Jakob disease; Huntington's chorea; viral
CC infections of the brain; brain tumours; lysosomal storage diseases;
CC Parkinson's disease; and multiple sclerosis. The present amino acid
CC sequence represents a protein which was used in the invention
XX
SQ Sequence 239 AA;

Query Match 79.2%; Score 1010.5; DB 6; Length 239;
Best Local Similarity 79.8%; Pred. No. 9.6e-60;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|| || :|| |||:||| |||:|| | |:|||||| |||||||:|: | | :||
Db          1 QVKLQESGAELVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
              ||||:||||:|||||||||||:|  |||||||:|:||||     |     |||||| |||||
Db         61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy        119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
              ||| ||||| |||||||||||||||||||||||||||||||:||||||||| ||||
Db        117 SSGGGGSGGVGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSP 176

Qy        179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
              |||||||||||||| |||||||| ||||||||:|||| |||| | | || ||| | ||
Db        177 KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPFTFGGGAKL 236

Qy        239 EIK 241
              |||
Db        237 EIK 239
```

RESULT 7
ADJ88113
ID ADJ88113 standard; protein; 239 AA.
XX
AC ADJ88113;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human beta amyloid peptide antibody (508) heavy chain protein.
XX
KW Neurological disease; central nervous system; CNS disorder;
KW plaque-forming disease; Alzheimer's disease; SAA amyloidosis;
KW hereditary Icelandic syndrome; senility; multiple myeloma; scrapie;
KW bovine spongiform encephalopathy; BSE; kuru; Creutzfeldt-Jakob disease;
KW CJD; Gerstmann-Streussler-Sheinker disease; GSS; fatal familial insomnia;
KW FFI; non-plaque-forming disease; Huntington's chorea; viral infection;
KW brain tumour; lysosomal storage disease; neurodegeneration;
KW multiple sclerosis; vaccine; beta amyloid peptide; beta AP; antibody;
KW human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 31. .35
FT /note= "CDR1"
FT Region 50. .66
FT /note= "CDR2"
FT Region 99. .107
FT /note= "CDR3"
XX
PN US2004013647-A1.
XX
PD 22-JAN-2004.
XX
PF 11-MAR-2003; 2003US-00384788.
XX
PR 03-SEP-1999; 99US-0152417P.
PR 29-DEC-1999; 99US-00473653.
PR 31-JUL-2000; 2000US-00629971.
PR 31-AUG-2000; 2000WO-IL000518.
PR 15-MAR-2001; 2001US-00808037.
PR 07-AUG-2001; 2001US-00830954.
PR 12-APR-2002; 2002US-0371735P.
PR 06-JUN-2002; 2002US-00162889.
XX
PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
XX
PI Solomon B, Frenkel D;
XX
DR WPI; 2004-108188/11.
DR N-PSDB; ADJ88112.
XX
PT Treating neurological disease CNS e.g., Alzheimer's disease, by
PT displaying therapeutic molecule capable of treating the disease on viral
PT display vehicle which is then administered to subject through olfactory
PT system.
XX
PS Example 2; SEQ ID NO 6; 68pp; English.
XX
CC The invention relates to a method of treating a neurological disease or
CC disorder of the central nervous system (CNS). The method involves
CC displaying a therapeutic molecule capable of treating the neurological
CC disease or disorder of the CNS on a viral display vehicle and introducing
CC viral display vehicle into a subject by applying an effective amount of
CC the viral display vehicle displaying the therapeutic molecule to an
CC olfactory system of the subject. The method is useful for treating a
CC neurological disease or disorder of CNS such as a plaque-forming disease
CC such as Alzheimer's disease, late onset Alzheimer's disease,
CC presymptomatic Alzheimer's disease, SAA amyloidosis, hereditary Icelandic
CC syndrome, senility, multiple myeloma, scrapie, bovine spongiform
CC encephalopathy (BSE), kuru, Creutzfeldt-Jakob disease (CJD), Gerstmann-
CC Streussler-Sheinker disease (GSS) or fatal familial insomnia (FFI). The
CC method is also useful for treating a non plaque forming disease or
CC disorder e.g. Huntington's chorea, viral infections of the brain, brain
CC tumours, lysosomal storage diseases which cause neurodegeneration and are
CC manifested by enzyme deficiencies and multiple sclerosis. The invention
CC is also used in the preparation of vaccines. The present sequence is
CC human beta amyloid peptide (beta AP) antibody heavy chain protein. This
CC sequence is used to illustrate the method of the invention.
XX
SQ Sequence 239 AA;

Query Match 79.2%; Score 1010.5; DB 8; Length 239;
Best Local Similarity 79.8%; Pred. No. 9.6e-60;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
```

```
              ||:||:|| || :|| |||:||| |||:|| | |:|||||| |||||||:|: | | :||
Db          1 QVKLQESGAELVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
               ||||:||||:|||||||||||:|  |||||||:|:||||    |    |||||| |||||
Db         61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy        119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
               ||| ||||| |||||||||||||||||||||||||||||||:||||||||| ||||
Db        117 SSGGGGSGGVGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSP 176

Qy        179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
               |||||||||||||| |||||||| ||||||||:|||| ||||| | | || ||| | ||
Db        177 KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPFTFGGGAKL 236

Qy        239 EIK 241
               |||
Db        237 EIK 239
```

RESULT 8
ADV66089
ID ADV66089 standard; protein; 494 AA.
XX
AC ADV66089;
XX
DT 24-FEB-2005 (first entry)
XX
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 12.
XX
KW bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS Unidentified.
XX
PN WO2004106383-A1.
XX
PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-EP005687.
XX
PR 31-MAY-2003; 2003EP-00012133.
PR 31-MAY-2003; 2003EP-00012134.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
XX
DR WPI; 2005-021271/02.
DR N-PSDB; ADV66088.
XX
PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 12; SEQ ID NO 12; 227pp; English.
XX
CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific
CC single chain antibody of the invention.
XX
SQ Sequence 494 AA;

Query Match 78.7%; Score 1004; DB 9; Length 494;
Best Local Similarity 80.3%; Pred. No. 5.5e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

```
Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::||||| || :|||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db          2 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 61

Qy         63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGV 122
              |||: ||||| ||||||||| | ||||||||||:|||   |    |||||||:|||||
Db         62 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSSGG 121

Qy        123 GGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWI 182
              ||||||||||||||:|||||||||||||||||| ||||||||:|||||||||||||
Db        122 GGSGGGGSGGGGSDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPKRWI 181

Qy        183 YDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              |||||:||||| |||||||| ||||||||:|||| ||||||||  |||||||||||:|
Db        182 YDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 240
```

RESULT 9
ADV66137
ID ADV66137 standard; protein; 500 AA.
XX
AC ADV66137;
XX
DT 24-FEB-2005 (first entry)
XX
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 60.
XX
KW bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS Unidentified.
XX
PN WO2004106383-A1.
XX
PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-EP005687.
XX
PR 31-MAY-2003; 2003EP-00012133.
PR 31-MAY-2003; 2003EP-00012134.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
XX
DR WPI; 2005-021271/02.
DR N-PSDB; ADV66136.
XX
PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 12; SEQ ID NO 60; 227pp; English.
XX
CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific
CC single chain antibody of the invention.
XX
SQ Sequence 500 AA;

Query Match 78.7%; Score 1004; DB 9; Length 500;
Best Local Similarity 80.3%; Pred. No. 5.6e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

```
Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::||||| || :|||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db          2 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 61
```

```
Qy          63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGV 122
               |||: ||||| ||||||||| | |||||||||:|||   |    ||||||||:|||||
Db          62 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSSGG 121

Qy         123 GGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWI 182
               ||||||||||||||:|||||||||||||||||| ||||||||:|||||||||||||||
Db         122 GGSGGGGSGGGGSDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPKRWI 181

Qy         183 YDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
               |||||:|||||| |||||||| |||||||||:|||| |||||||||  ||||||||||:|
Db         182 YDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 240


RESULT 10
ADV66095
ID   ADV66095 standard; protein; 500 AA.
XX
AC   ADV66095;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 18.
XX
KW   bispecific single chain antibody; epithelial cell adhesion molecule;
KW   EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS   Unidentified.
XX
PN   WO2004106383-A1.
XX
PD   09-DEC-2004.
XX
PF   26-MAY-2004; 2004WO-EP005687.
XX
PR   31-MAY-2003; 2003EP-00012133.
PR   31-MAY-2003; 2003EP-00012134.
XX
PA   (MICR-) MICROMET AG.
XX
PI   Kufer P,  Berry M,  Offner S,  Brischwein K,  Wolf A,  Raum T;
PI   Kohleisen B,  Lenkkeri-Schuetz U,  Baeuerle P;
XX
DR   WPI; 2005-021271/02.
DR   N-PSDB; ADV66094.
XX
PT   New pharmaceutical composition having a bispecific single chain antibody
PT   construct, useful for preventing, treating or ameliorating a tumorous
PT   disease, such as an epithelial or minimal residual cancer.
XX
PS   Claim 12; SEQ ID NO 18; 227pp; English.
XX
CC   The invention comprises a composition that contains a bispecific single
CC   chain antibody consisting of at least two domains, where one of domains
CC   binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC   second domain binds to human CD3 antigen. The bispecific antibody
CC   construct of the invention is useful for the prevention, treatment or
CC   amelioration of a tumorous disease, such as an epithelial or minimal
CC   residual cancer. The present amino acid sequence represents a bispecific
CC   single chain antibody of the invention.
XX
SQ   Sequence 500 AA;

  Query Match             78.7%;  Score 1004;  DB 9;  Length 500;
  Best Local Similarity   80.3%;  Pred. No. 5.6e-59;
  Matches  192;  Conservative   17;  Mismatches   30;  Indels    0;  Gaps    0;

Qy           3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
               ::||||| || :||||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db           2 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 61

Qy          63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGV 122
               |||: ||||| ||||||||| | |||||||||:|||   |    ||||||||:|||||
Db          62 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSSGG 121

Qy         123 GGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWI 182
               ||||||||||||||:|||||||||||||||||| ||||||||:|||||||||||||||
Db         122 GGSGGGGSGGGGSDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPKRWI 181

Qy         183 YDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
               |||||:|||||| |||||||| |||||||||:|||| |||||||||  ||||||||||:|
Db         182 YDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 240


RESULT 11
ADV66097
ID   ADV66097 standard; protein; 500 AA.
XX
AC   ADV66097;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 20.
XX
KW   bispecific single chain antibody; epithelial cell adhesion molecule;
KW   EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS   Unidentified.
XX
PN   WO2004106383-A1.
XX
PD   09-DEC-2004.
XX
PF   26-MAY-2004; 2004WO-EP005687.
XX
PR   31-MAY-2003; 2003EP-00012133.
PR   31-MAY-2003; 2003EP-00012134.
XX
PA   (MICR-) MICROMET AG.
XX
PI   Kufer P,  Berry M,  Offner S,  Brischwein K,  Wolf A,  Raum T;
PI   Kohleisen B,  Lenkkeri-Schuetz U,  Baeuerle P;
XX
DR   WPI; 2005-021271/02.
DR   N-PSDB; ADV66096.
XX
PT   New pharmaceutical composition having a bispecific single chain antibody
PT   construct, useful for preventing, treating or ameliorating a tumorous
PT   disease, such as an epithelial or minimal residual cancer.
XX
PS   Claim 12; SEQ ID NO 20; 227pp; English.
XX
CC   The invention comprises a composition that contains a bispecific single
CC   chain antibody consisting of at least two domains, where one of domains
CC   binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC   second domain binds to human CD3 antigen. The bispecific antibody
CC   construct of the invention is useful for the prevention, treatment or
CC   amelioration of a tumorous disease, such as an epithelial or minimal
CC   residual cancer. The present amino acid sequence represents a bispecific
CC   single chain antibody of the invention.
XX
SQ   Sequence 500 AA;

  Query Match             78.7%;  Score 1004;  DB 9;  Length 500;
  Best Local Similarity   80.3%;  Pred. No. 5.6e-59;
  Matches  192;  Conservative   17;  Mismatches   30;  Indels    0;  Gaps    0;

Qy           3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
               ::||||| || :||||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db           2 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 61

Qy          63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGV 122
               |||: ||||| ||||||||| | |||||||||:|||   |    ||||||||:|||||
Db          62 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSSGG 121

Qy         123 GGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWI 182
```

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                ||||||||||||||||:|||||||||||||||||||| ||||||||:|||||||||||||||
Db        122 GGSGGGGSGGGGSDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPKRWI 181

Qy        183 YDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
                |||||:||||| |||||||| ||||||||:|||| |||||||||  ||||||||||:|
Db        182 YDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 240


RESULT 12
ADV66131
ID   ADV66131 standard; protein; 503 AA.
XX
AC   ADV66131;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 54.
XX
KW   bispecific single chain antibody; epithelial cell adhesion molecule;
KW   EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS   Unidentified.
XX
PN   WO2004106383-A1.
XX
PD   09-DEC-2004.
XX
PF   26-MAY-2004; 2004WO-EP005687.
XX
PR   31-MAY-2003; 2003EP-00012133.
PR   31-MAY-2003; 2003EP-00012134.
XX
PA   (MICR-) MICROMET AG.
XX
PI   Kufer P,  Berry M,  Offner S,  Brischwein K,  Wolf A,  Raum T;
PI   Kohleisen B,  Lenkkeri-Schuetz U,  Baeuerle P;
XX
DR   WPI; 2005-021271/02.
DR   N-PSDB; ADV66130.
XX
PT   New pharmaceutical composition having a bispecific single chain antibody
PT   construct, useful for preventing, treating or ameliorating a tumorous
PT   disease, such as an epithelial or minimal residual cancer.
XX
PS   Claim 12; SEQ ID NO 54; 227pp; English.
XX
CC   The invention comprises a composition that contains a bispecific single
CC   chain antibody consisting of at least two domains, where one of domains
CC   binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC   second domain binds to human CD3 antigen. The bispecific antibody
CC   construct of the invention is useful for the prevention, treatment or
CC   amelioration of a tumorous disease, such as an epithelial or minimal
CC   residual cancer. The present amino acid sequence represents a bispecific
CC   single chain antibody of the invention.
XX
SQ   Sequence 503 AA;

  Query Match             78.7%;  Score 1004;  DB 9;  Length 503;
  Best Local Similarity   80.3%;  Pred. No. 5.6e-59;
  Matches  192;  Conservative   17;  Mismatches   30;  Indels    0;  Gaps    0;

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Db          2 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 61

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Qy        183 YDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
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RESULT 13
ADV66093
ID   ADV66093 standard; protein; 503 AA.
XX
AC   ADV66093;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 16.
XX
KW   bispecific single chain antibody; epithelial cell adhesion molecule;
KW   EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS   Unidentified.
XX
PN   WO2004106383-A1.
XX
PD   09-DEC-2004.
XX
PF   26-MAY-2004; 2004WO-EP005687.
XX
PR   31-MAY-2003; 2003EP-00012133.
PR   31-MAY-2003; 2003EP-00012134.
XX
PA   (MICR-) MICROMET AG.
XX
PI   Kufer P,  Berry M,  Offner S,  Brischwein K,  Wolf A,  Raum T;
PI   Kohleisen B,  Lenkkeri-Schuetz U,  Baeuerle P;
XX
DR   WPI; 2005-021271/02.
DR   N-PSDB; ADV66092.
XX
PT   New pharmaceutical composition having a bispecific single chain antibody
PT   construct, useful for preventing, treating or ameliorating a tumorous
PT   disease, such as an epithelial or minimal residual cancer.
XX
PS   Claim 12; SEQ ID NO 16; 227pp; English.
XX
CC   The invention comprises a composition that contains a bispecific single
CC   chain antibody consisting of at least two domains, where one of domains
CC   binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC   second domain binds to human CD3 antigen. The bispecific antibody
CC   construct of the invention is useful for the prevention, treatment or
CC   amelioration of a tumorous disease, such as an epithelial or minimal
CC   residual cancer. The present amino acid sequence represents a bispecific
CC   single chain antibody of the invention.
XX
SQ   Sequence 503 AA;

  Query Match             78.7%;  Score 1004;  DB 9;  Length 503;
  Best Local Similarity   80.3%;  Pred. No. 5.6e-59;
  Matches  192;  Conservative   17;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::|||||  || :|||||||:||| |||:|| |||:|||| |: |||||  | |  | ::||
Db          2 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 61

Qy         63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGV 122
              |||: |||||  |||||||||  | ||||||||||:|||    |     ||||||||:|||||
Db         62 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSSGG 121

Qy        123 GGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWI 182
              ||||||||||||||:|||||||||||||||||||| ||||||||:|||||||||||||||
Db        122 GGSGGGGSGGGGSDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPKRWI 181

Qy        183 YDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              |||||:||||| |||||||| ||||||||:|||| |||||||||  ||||||||||:|
Db        182 YDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 240
```

RESULT 14
ADV66091
ID ADV66091 standard; protein; 503 AA.
XX
AC ADV66091;
XX
DT 24-FEB-2005 (first entry)
XX
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 14.
XX
KW bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS Unidentified.
XX
PN WO2004106383-A1.
XX
PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-EP005687.
XX
PR 31-MAY-2003; 2003EP-00012133.
PR 31-MAY-2003; 2003EP-00012134.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
XX
DR WPI; 2005-021271/02.
DR N-PSDB; ADV66090.
XX
PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 12; SEQ ID NO 14; 227pp; English.
XX
CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific
CC single chain antibody of the invention.
XX
SQ Sequence 503 AA;

Query Match 78.7%; Score 1004; DB 9; Length 503;
Best Local Similarity 80.3%; Pred. No. 5.6e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

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Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::||||| || :||||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db          2 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 61

Qy         63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGV 122
              |||: ||||| ||||||||| | ||||||||||:|||   |    ||||||||:|||||
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Qy        123 GGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWI 182
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Qy        183 YDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              |||||:||||| |||||||| |||||||||:|||| |||||||||  ||||||||||:|
Db        182 YDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 240
```

RESULT 15

ADV14540
ID ADV14540 standard; protein; 503 AA.
XX
AC ADV14540;
XX
DT 24-FEB-2005 (first entry)
XX
DE Bispecific VH(CD3)-VL(CD3)-VL(CD19)-VH(CD19) antibody protein Seq 14.
XX
KW bispecific antibody; antibody engineering; antibody therapy; CD3; CD19;
KW proliferative disorders; cancer; tumor; B-cell leukemia; inflammation;
KW immune disorder; autoimmune disease; rheumatoid arthritis;
KW viral infection; allergy; parasitic infection; graft-versus-host disease;
KW cytostatic; antiinflammatory; immunosuppressive; antimicrobial-gen.;
KW antirheumatic; antiarthritic; virucide; antiparasitic; antiallergic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004106381-A1.
XX
PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-EP005685.
XX
PR 31-MAY-2003; 2003EP-00012136.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Lutterbuese R, Kohleisen B, Zeman S, Baeuerle P;
XX
DR WPI; 2005-021270/02.
DR N-PSDB; ADV14539.
XX
PT Use of bispecific single chain antibody construct, nucleic acid sequence
PT encoding the antibody construct, vector containing the nucleic acid or
PT host transformed with the vector for the treatment of e.g. proliferative
PT and autoimmune disease.
XX
PS Claim 9; SEQ ID NO 14; 115pp; English.
XX
CC This invention relates to novel pharmaceutical compositions that comprise
CC a bispecific single chain antibody construct, a nucleic acid sequence
CC encoding the antibody construct and a vector that contains the nucleic
CC acid sequence. Specifically, it refers to an antibody construct that
CC contains binding domains specific for the human T cell differentiation
CC antigens CD3 and CD19, with specific variable heavy and light chain
CC regions. In particular such constructs include, from the N- to C-termini,
CC in the order, VH(CD19)-VL(CD19)-VH(CD3)-VL(CD3), VH(CD3)-VL(CD3)-VH(CD19)
CC -VL(CD19), or VH(CD3)-VL(CD3)-VL(CD19)-VH(CD19). The present invention
CC describes a method of culturing the host transformed with this vector in
CC order to recover expressed bispecific single chain antibodies from the
CC culture solution. Note that the pharmaceutical composition additionally
CC comprises a proteinaceous compound that provides an activation signal for
CC immune effector cells. Furthermore, this invention provides compositions
CC that can be used for the treatment, prevention or amelioration of
CC proliferative disease, minimal residual cancer, tumorous disease (e.g. B-
CC cell leukemia), inflammatory disease, immunological disorder, autoimmune
CC disease (e.g. rheumatoid arthritis), infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, host
CC -versus-graft diseases and B-cell malignancies. As such, these
CC compositions exhibit cytostatic, antiinflammatory, immunosuppressive,
CC antimicrobial, antirheumatic, antiarthritic, virucide, antiparasitic and
CC antiallergic activities. In addition, these compositions provide well-
CC tolerated and convenient medicaments that are highly active and potent at
CC low concentrations and as such avoid adverse side effects including
CC hypersensitivity and inflammatory events caused by excessive protein
CC concentrations. This polypeptide sequence is a bispecific single chain
CC antibody protein that targets human CD3 and CD19 antigens, as given in an
CC exemplification of the invention.
XX
SQ Sequence 503 AA;

Query Match 78.7%; Score 1004; DB 9; Length 503;
Best Local Similarity 80.3%; Pred. No. 5.6e-59;
Matches 192; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

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Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::|||||  ||  :||||||:|||  |||:||  |||:||||   |: |||||  | |   | ::||
Db          2 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 61

Qy         63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSGV 122
              |||: |||||  |||||||||  |  ||||||||||:|||    |     |||||||:|||||
Db         62 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSSGG 121

Qy        123 GGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWI 182
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Db        122 GGSGGGGSGGGGSDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPKRWI 181

Qy        183 YDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
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Job time : 324 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 3, 2006, 05:30:32 ; Search time 61 Seconds
(without alignments)
1650.768 Million cell updates/sec

Title: US-09-979-539-1
Perfect score: 1276
Sequence: 1 MQVQLQQSGPELEKPGASVK.....CQQWSGYPLTFGAGTKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1274	99.8	241	5	US-10-973-718-5	Sequence 5, Appli
2	1025.5	80.4	242	4	US-10-259-087A-20	Sequence 20, Appl
3	1025.5	80.4	242	4	US-10-689-006-20	Sequence 20, Appl
4	1010.5	79.2	239	3	US-09-808-037-6	Sequence 6, Appli
5	1010.5	79.2	239	4	US-10-162-889-6	Sequence 6, Appli
6	1010.5	79.2	239	4	US-10-384-788-6	Sequence 6, Appli
7	1010.5	79.2	239	4	US-10-618-856-6	Sequence 6, Appli
8	1010.5	79.2	239	5	US-10-749-522-6	Sequence 6, Appli
9	1010.5	79.2	239	6	US-11-073-526-6	Sequence 6, Appli
10	1003	78.6	261	4	US-10-689-006-24	Sequence 24, Appl
11	989.5	77.5	242	4	US-10-259-087A-18	Sequence 18, Appl
12	989.5	77.5	242	4	US-10-689-006-18	Sequence 18, Appl
13	967.5	75.8	492	4	US-10-682-845-63	Sequence 63, Appl
14	967.5	75.8	492	4	US-10-682-845-79	Sequence 79, Appl
15	967.5	75.8	492	4	US-10-682-845-83	Sequence 83, Appl
16	966.5	75.7	492	4	US-10-682-845-87	Sequence 87, Appl
17	966	75.7	246	5	US-10-861-617-15	Sequence 15, Appl
18	965.5	75.7	492	4	US-10-682-845-61	Sequence 61, Appl
19	965.5	75.7	492	4	US-10-682-845-71	Sequence 71, Appl
20	965.5	75.7	492	4	US-10-682-845-73	Sequence 73, Appl
21	965.5	75.7	492	4	US-10-682-845-77	Sequence 77, Appl
22	964.5	75.6	243	5	US-10-966-406-2	Sequence 2, Appli
23	964.5	75.6	409	4	US-10-362-591-2	Sequence 2, Appli
24	964.5	75.6	492	4	US-10-682-845-59	Sequence 59, Appl
25	964.5	75.6	492	4	US-10-682-845-67	Sequence 67, Appl
26	964.5	75.6	492	4	US-10-682-845-69	Sequence 69, Appl
27	964.5	75.6	499	5	US-10-805-177-111	Sequence 111, App
28	964.5	75.6	500	4	US-10-168-809-22	Sequence 22, Appl
29	963.5	75.5	492	4	US-10-682-845-75	Sequence 75, Appl
30	963.5	75.5	492	4	US-10-682-845-85	Sequence 85, Appl
31	962.5	75.4	260	4	US-10-435-614-20	Sequence 20, Appl
32	961	75.3	246	5	US-10-861-617-17	Sequence 17, Appl
33	961	75.3	657	5	US-10-723-003-48	Sequence 48, Appl
34	961	75.3	657	6	US-11-004-639-48	Sequence 48, Appl
35	960.5	75.3	492	4	US-10-682-845-65	Sequence 65, Appl
36	959.5	75.2	256	4	US-10-247-488-2	Sequence 2, Appli
37	959.5	75.2	258	4	US-10-247-488-4	Sequence 4, Appli
38	957.5	75.0	492	4	US-10-682-845-81	Sequence 81, Appl
39	956.5	75.0	495	3	US-09-948-004-18	Sequence 18, Appl
40	956.5	75.0	495	5	US-10-672-932-18	Sequence 18, Appl
41	956	74.9	281	4	US-10-112-788-9	Sequence 9, Appli
42	956	74.9	281	4	US-10-435-614-15	Sequence 15, Appl
43	950	74.5	438	4	US-10-244-821-88	Sequence 88, Appl
44	948.5	74.3	260	4	US-10-435-614-19	Sequence 19, Appl
45	941.5	73.8	423	4	US/10/013	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-973-718-5
; Sequence 5, Application US/10973718
; Publication No. US20050214304A1
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Chowdhury, Partha S.
; APPLICANT: The Government of the United States
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Antibodies, Including Fv Molecules, and
; TITLE OF INVENTION: Immunoconjugates Having High Binding Affinity for
; TITLE OF INVENTION: Mesothelin and Methods for Their Use
; FILE REFERENCE: 015280-339100US
; CURRENT APPLICATION NUMBER: US/10/973,718
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: US/09/581,345
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/067,175
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: WO PCT/US98/25270
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SS scFv
US-10-973-718-5

Query Match 99.8%; Score 1274; DB 5; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.2e-82;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240

Qy        241 K 241
              |
Db        241 K 241


RESULT 2
US-10-259-087A-20
; Sequence 20, Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
;  APPLICANT: Vanderbilt University
;  APPLICANT:  Hallahan, Dennis E
;  APPLICANT:  Qu, Shimian
;  TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
;  FILE REFERENCE: 1242/47/2
;  CURRENT APPLICATION NUMBER: US/10/259,087A
;  CURRENT FILING DATE:  2002-09-27
;  PRIOR APPLICATION NUMBER: US 60/328123
;  PRIOR FILING DATE: 2001-10-03
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial antibody ligand number 2
US-10-259-087A-20

  Query Match             80.4%;  Score 1025.5;  DB 4;  Length 242;
  Best Local Similarity   81.7%;  Pred. No. 5.2e-65;
  Matches  196;  Conservative   13;  Mismatches   30;  Indels    1;  Gaps    1;

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Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
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Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
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RESULT 3
US-10-689-006-20
; Sequence 20, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
;  APPLICANT: Vanderbilt University
;  APPLICANT:  Hallahan, Dennis E
;  APPLICANT:  Mernaugh, Raymond
;  TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
;  FILE REFERENCE: 1242/72
;  CURRENT APPLICATION NUMBER: US/10/689,006
;  CURRENT FILING DATE:  2003-10-20
;  PRIOR APPLICATION NUMBER: US 09/914,605
;  PRIOR FILING DATE: 2001-08-30
;  PRIOR APPLICATION NUMBER: US 10/259,087
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Artificial antibody ligand number 2
US-10-689-006-20

  Query Match             80.4%;  Score 1025.5;  DB 4;  Length 242;
  Best Local Similarity   81.7%;  Pred. No. 5.2e-65;
  Matches  196;  Conservative   13;  Mismatches   30;  Indels    1;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:|||||||| |||||||:|||||||:|| | |:|||| |: ||||| | ||| : |
Db          3 QVKLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              |:||:||| || ||||||||:| ||||||||||:||| |  |   ||||||||||||||
Db         63 NEKFKGKAALTSDKSSSTAYMELSSLTSEDSAVYYCARFGNYG-ALDYWGQGTTVTVSSG 121

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              |||||||||||||||||||| |||||||||||:|||||||||||:||| ||||| |
Db        122 GGGSGGGGSGGGGSDIELTQSPTIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKPW 181

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              || || |||||| |||||||| ||||||||:|||| ||||||||| |||||| |||||||
Db        182 IYGTSNLASGVPVRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSYPLTFGGGTKLEIK 241


RESULT 4
US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
;  APPLICANT: SOLOMON, Beka
;  APPLICANT:  HANAN, Eilat
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
;  TITLE OF INVENTION:  NEUROLOGICAL DISEASES AND DISORDERS
;  FILE REFERENCE: SOLOMON=2D
;  CURRENT APPLICATION NUMBER: US/09/808,037
;  CURRENT FILING DATE:  2001-03-15
;  PRIOR APPLICATION NUMBER: 09/629,971
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/473,653
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: US 60/152,417
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-808-037-6

  Query Match             79.2%;  Score 1010.5;  DB 3;  Length 239;
  Best Local Similarity   79.8%;  Pred. No. 6e-64;
  Matches  194;  Conservative   16;  Mismatches   26;  Indels    7;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|| || :|| |||:||| |||:|| | |:|||||| ||||||||:|: | | :||
Db          1 QVKLQESGAELVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
              ||||:||||:|||||||||||:|  |||||||:|:||||     |     |||||| |||||
Db         61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy        119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
              ||| ||||| |||||||||||||||||||||||||||||||||:||||||||| ||||
Db        117 SSGGGGSGGVGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSP 176

Qy        179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
              ||||||||||||||| |||||||| ||||||||:|||| ||||| | | || ||| | ||
Db        177 KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPFTFGGGAKL 236

Qy        239 EIK 241
```

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Db        237 EIK 239


RESULT 5
US-10-162-889-6
; Sequence 6, Application US/10162889
; Publication No. US20030077252A1
; GENERAL INFORMATION:
;  APPLICANT: SOLOMON, Beka
;  APPLICANT:  HANAN, Eilat
;  TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
;  TITLE OF INVENTION:  USEFUL IN DIAGNOSING
;  TITLE OF INVENTION:  AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
;  FILE REFERENCE: SOLOMON=2B
;  CURRENT APPLICATION NUMBER: US/10/162,889
;  CURRENT FILING DATE:  2002-06-06
;  PRIOR APPLICATION NUMBER: US/09/629,971
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/473,653
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: US 60/152,417
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-162-889-6

  Query Match             79.2%;  Score 1010.5;  DB 4;  Length 239;
  Best Local Similarity   79.8%;  Pred. No. 6e-64;
  Matches  194;  Conservative   16;  Mismatches   26;  Indels    7;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|| || :|| |||:||| |||:|| | |:|||||| |||||||:|: | | :||
Db          1 QVKLQESGAELVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
              ||||:||||:||||||||||:|  |||||||:|:||||    |    |||||| |||||
Db         61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy        119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
              ||| ||||| ||||||||||||||||||||||||||||||:|||||||| ||||
Db        117 SSGGGGSGGVGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSP 176

Qy        179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
              |||||||||||||| |||||||| ||||||||:|||| ||||| | | || ||| | ||
Db        177 KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPFTFGGGAKL 236

Qy        239 EIK 241
              |||
Db        237 EIK 239


RESULT 6
US-10-384-788-6
; Sequence 6, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
;  APPLICANT: SOLOMON, Beka
;  APPLICANT:  FRENKEL, Dan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
;  FILE REFERENCE: SOLOMON=2D.2
;  CURRENT APPLICATION NUMBER: US/10/384,788
;  CURRENT FILING DATE:  2003-03-11
;  PRIOR APPLICATION NUMBER: 60/371,735
;  PRIOR FILING DATE: 2002-04-12
;  PRIOR APPLICATION NUMBER: 09/808,037
;  PRIOR FILING DATE: 2001-03-15
;  PRIOR APPLICATION NUMBER: 09/830,954
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 10/162,889
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: 09/473,653
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 09/629,971
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: 60/152,417
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: PCT/IL00/00518
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-384-788-6

  Query Match             79.2%;  Score 1010.5;  DB 4;  Length 239;
  Best Local Similarity   79.8%;  Pred. No. 6e-64;
  Matches  194;  Conservative   16;  Mismatches   26;  Indels    7;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|| || :|| |||:||| |||:|| | |:|||||| |||||||:|: | | :||
Db          1 QVKLQESGAELVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
              ||||:||||:||||||||||:|  |||||||:|:||||    |    |||||| |||||
Db         61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy        119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
              ||| ||||| ||||||||||||||||||||||||||||||:|||||||| ||||
Db        117 SSGGGGSGGVGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSP 176

Qy        179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
              |||||||||||||| |||||||| ||||||||:|||| ||||| | | || ||| | ||
Db        177 KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPFTFGGGAKL 236

Qy        239 EIK 241
              |||
Db        237 EIK 239


RESULT 7
US-10-618-856-6
; Sequence 6, Application US/10618856
; Publication No. US20040052766A1
; GENERAL INFORMATION:
;  APPLICANT: SOLOMON, Beka
;  APPLICANT:  FRENKEL, Dan
;  TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
;  FILE REFERENCE: SOLOMON=2A
;  CURRENT APPLICATION NUMBER: US/10/618,856
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/473,653A
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: US 60/152,417
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-618-856-6

  Query Match             79.2%;  Score 1010.5;  DB 4;  Length 239;
  Best Local Similarity   79.8%;  Pred. No. 6e-64;
  Matches  194;  Conservative   16;  Mismatches   26;  Indels    7;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|| || :|| |||:||| |||:|| | |:|||||| |||||||:|: | | :||
Db          1 QVKLQESGAELVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60
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Qy          62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
               ||||:||||:|||||||||||:|  |||||||:|:||||    |    |||||| |||||
Db          61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy         119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
               ||| ||||| ||||||||||||||||||||||||||||||||||:||||||||| ||||
Db         117 SSGGGGSGGVGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSP 176

Qy         179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
               |||||||||||||| |||||||| ||||||||:|||| |||||| | | || ||| | ||
Db         177 KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPFTFGGGAKL 236

Qy         239 EIK 241
               |||
Db         237 EIK 239
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RESULT 8
US-10-749-522-6
; Sequence 6, Application US/10749522
; Publication No. US20050089510A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON=2B
; CURRENT APPLICATION NUMBER: US/10/749,522
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-749-522-6

Query Match 79.2%; Score 1010.5; DB 5; Length 239;
Best Local Similarity 79.8%; Pred. No. 6e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

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Qy           2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
               ||:||:|| || :|| |||:||| |||:|| | |:|||||| |||||||:|: | | :||
Db           1 QVKLQESGAELVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60

Qy          62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
               ||||:||||:|||||||||||:|  |||||||:|:||||    |    |||||| |||||
Db          61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy         119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
               ||| ||||| ||||||||||||||||||||||||||||||||||:||||||||| ||||
Db         117 SSGGGGSGGVGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSP 176

Qy         179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
               |||||||||||||| |||||||| ||||||||:|||| |||||| | | || ||| | ||
Db         177 KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPFTFGGGAKL 236

Qy         239 EIK 241
               |||
Db         237 EIK 239
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RESULT 9
US-11-073-526-6
; Sequence 6, Application US/11073526
; Publication No. US20050152878A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: FRENKEL, Dan
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIA
; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON=2C
; CURRENT APPLICATION NUMBER: US/11/073,526
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/830,954
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-526-6

Query Match 79.2%; Score 1010.5; DB 6; Length 239;
Best Local Similarity 79.8%; Pred. No. 6e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

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Qy           2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
               ||:||:|| || :|| |||:||| |||:|| | |:|||||| |||||||:|: | | :||
Db           1 QVKLQESGAELVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYYGDASY 60

Qy          62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
               ||||:||||:|||||||||||:|  |||||||:|:||||    |    |||||| |||||
Db          61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy         119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
               ||| ||||| ||||||||||||||||||||||||||||||||||:||||||||| ||||
Db         117 SSGGGGSGGVGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSP 176

Qy         179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
               |||||||||||||| |||||||| ||||||||:|||| |||||| | | || ||| | ||
Db         177 KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPFTFGGGAKL 236

Qy         239 EIK 241
               |||
Db         237 EIK 239
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RESULT 10
US-10-689-006-24
; Sequence 24, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 261
; TYPE: PRT

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;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: nucleic acid encoding scFv antibody 10A
US-10-689-006-24

  Query Match             78.6%;  Score 1003;  DB 4;  Length 261;
  Best Local Similarity   80.9%;  Pred. No. 2.2e-63;
  Matches  195;  Conservative   17;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:|||||||| |||||||:|||||||:|| | |:|||||:|||||||| | || | :||
Db          3 QVKLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQSNGKSLEWIGTIDPYYGGTSY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCAR-GGYDGRGPDYWGQGTTVTVSS 120
              ||||:||||||||||:|||: | ||||||||||:|||  || | || |||||| |||||
Db         63 NQKFKGKATLTVDKSSTTAYIQLKSLTSEDSAVYYCARWDGYYG-GFSYWGQGTMVTVSS 121

Qy        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKR 180
              | |||||||||||||||||||||||||: ||||||:| |||:| ||:||||||| |||
Db        122 GGGGSGGGGSGGGGSDIELTQSPAIMSATLGEKVTMSCRASSNVKYMYWYQQKSGASPKL 181

Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
              ||| || |||||| |||||||| |||||||||||| |||||||::  | |||:||||||
Db        182 WIYYTSNLASGVPARFSGSGSGTSYSLTISSVEAEDAATYYCQQFTSSPYTFGSGTKLEI 241

Qy        241 K 241
              |
Db        242 K 242


RESULT 11
US-10-259-087A-18
; Sequence 18, Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
;  APPLICANT: Vanderbilt University
;  APPLICANT:  Hallahan, Dennis E
;  APPLICANT:  Qu, Shimian
;  TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
;  FILE REFERENCE: 1242/47/2
;  CURRENT APPLICATION NUMBER: US/10/259,087A
;  CURRENT FILING DATE:  2002-09-27
;  PRIOR APPLICATION NUMBER: US 60/328123
;  PRIOR FILING DATE: 2001-10-03
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial antibody ligand number 1
US-10-259-087A-18

  Query Match             77.5%;  Score 989.5;  DB 4;  Length 242;
  Best Local Similarity   80.4%;  Pred. No. 1.9e-62;
  Matches  193;  Conservative   14;  Mismatches   32;  Indels    1;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||||| ||  ||||||:|||||||:|| | |:||||  |: ||||| |   :  :||
Db          3 QVKLQQSGAELVMPGASVKMSCKASGYTFTDYWMHWVKQRPGQGLEWIGAIDTSDSYTSY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              ||||:||||||||:||||||| | |||||||||||:||| ||    ||||||||||||||
Db         63 NQKFKGKATLTVDESSSTAYMQLSSLTSEDSAVYYCARRGYYS-AFDYWGQGTTVTVSSG 121

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
               |||||||||||||||||||  |:||||||||:|| ||||||||||:||||||||| |
Db        122 GGGSGGGGSGGGGSDIELTQSPTTMAASPGEKVTITCRASSSVSYMHWFQQKSGTSPKPW 181

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              |||||||||||| |||||||| ||||||||:|||| ||||| | | || ||||||||||||
Db        182 IYDTSKLASGVPDRFSGSGSGTSYSLTISSMEAEDAATYYCLQRSSYPYTFGAGTKLEIK 241


RESULT 12
US-10-689-006-18
; Sequence 18, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
;  APPLICANT: Vanderbilt University
;  APPLICANT:  Hallahan, Dennis E
;  APPLICANT:  Mernaugh, Raymond
;  TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
;  FILE REFERENCE: 1242/72
;  CURRENT APPLICATION NUMBER: US/10/689,006
;  CURRENT FILING DATE:  2003-10-20
;  PRIOR APPLICATION NUMBER: US 09/914,605
;  PRIOR FILING DATE: 2001-08-30
;  PRIOR APPLICATION NUMBER: US 10/259,087
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Artificial antibody ligand number 1
US-10-689-006-18

  Query Match             77.5%;  Score 989.5;  DB 4;  Length 242;
  Best Local Similarity   80.4%;  Pred. No. 1.9e-62;
  Matches  193;  Conservative   14;  Mismatches   32;  Indels    1;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||||| ||  ||||||:|||||||:|| | |:||||  |: ||||| |   :  :||
Db          3 QVKLQQSGAELVMPGASVKMSCKASGYTFTDYWMHWVKQRPGQGLEWIGAIDTSDSYTSY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              ||||:||||||||:||||||| | |||||||||||:||| ||    ||||||||||||||
Db         63 NQKFKGKATLTVDESSSTAYMQLSSLTSEDSAVYYCARRGYYS-AFDYWGQGTTVTVSSG 121

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
               |||||||||||||||||||  |:||||||||:|| ||||||||||:||||||||| |
Db        122 GGGSGGGGSGGGGSDIELTQSPTTMAASPGEKVTITCRASSSVSYMHWFQQKSGTSPKPW 181

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              |||||||||||| |||||||| ||||||||:|||| ||||| | | || ||||||||||||
Db        182 IYDTSKLASGVPDRFSGSGSGTSYSLTISSMEAEDAATYYCLQRSSYPYTFGAGTKLEIK 241


RESULT 13
US-10-682-845-63
; Sequence 63, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
;  APPLICANT: Lanzavecchia, Antonio
;  TITLE OF INVENTION: Potent T cell modulating molecules
;  FILE REFERENCE: G2296 US
;  CURRENT APPLICATION NUMBER: US/10/682,845
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: US 60/419,149
;  PRIOR FILING DATE: 2002-10-18
;  PRIOR APPLICATION NUMBER: CA 2,403,313
;  PRIOR FILING DATE: 2002-10-11
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 492
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: scFv EpCAMxCD3 with M4 mutant in anti-CD3 part
US-10-682-845-63
```

Query Match 75.8%; Score 967.5; DB 4; Length 492;
Best Local Similarity 77.3%; Pred. No. 1.4e-60;
Matches 187; Conservative 17; Mismatches 35; Indels 3; Gaps 1;

```
Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::||||| || :||||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db        245 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 304

Qy         63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS-- 120
              |||: ||||| ||||||||| | ||||||||||:|||   |    ||||||||:||||
Db        305 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYSDDHYCLDYWGQGTTLTVSSVE 364

Qy        121 -GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPK 179
               | ||||| |  ||  ||:||||||||||||||||||| ||||||||:||||||||||
Db        365 GGSGGSGGSGGSGGVDDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPK 424

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
              ||||||||:||||| |||||||| |||||||||:|||| |||||||||  ||||||||||
Db        425 RWIYDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 484

Qy        240 IK 241
              :|
Db        485 LK 486
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RESULT 14
US-10-682-845-79
; Sequence 79, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M31 mutant in anti-CD3 part
US-10-682-845-79

Query Match 75.8%; Score 967.5; DB 4; Length 492;
Best Local Similarity 77.8%; Pred. No. 1.4e-60;
Matches 189; Conservative 18; Mismatches 31; Indels 5; Gaps 3;

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Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::||||| || :||||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db        245 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 304

Qy         63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGR-GFDYWGQGTTVTVSS- 120
              |||: ||||| ||||||||| | ||||||||||:|||  |:||   ||||||||:||||
Db        305 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCAR-YYEGRYCLDYWGQGTTLTVSSV 363

Qy        121 --GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
                | ||||| |  ||  ||:||||||||||||||||||| ||||||||:||||||||||
Db        364 EGGSGGSGGSGGSGGVDDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSP 423

Qy        179 KRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
              |||||||||:||||| |||||||| |||||||||:|||| |||||||||  ||||||||||
Db        424 KRWIYDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKL 483

Qy        239 EIK 241
              |:|
Db        484 ELK 486
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RESULT 15
US-10-682-845-83
; Sequence 83, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M65 mutant in anti-CD3 part
US-10-682-845-83

Query Match 75.8%; Score 967.5; DB 4; Length 492;
Best Local Similarity 77.3%; Pred. No. 1.4e-60;
Matches 187; Conservative 17; Mismatches 35; Indels 3; Gaps 1;

```
Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::||||| || :||||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db        245 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 304

Qy         63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS-- 120
              |||: ||||| ||||||||| | ||||||||||:|||   |    ||||||||:||||
Db        305 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYSDDRYCLDYWGQGTTLTVSSVE 364

Qy        121 -GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPK 179
               | ||||| |  ||  ||:||||||||||||||||||| ||||||||:||||||||||
Db        365 GGSGGSGGSGGSGGVDDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPK 424

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
              ||||||||:||||| |||||||| |||||||||:|||| |||||||||  ||||||||||
Db        425 RWIYDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 484

Qy        240 IK 241
              :|
Db        485 LK 486
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Search completed: April 3, 2006, 05:33:08
Job time : 62 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 3, 2006, 05:30:32 ; Search time 45 Seconds
(without alignments)
163.033 Million cell updates/sec

Title: US-09-979-539-1
Perfect score: 1276
Sequence: 1 MQVQLQQSGPELEKPGASVK.....CQQWSGYPLTFGAGTKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	964.5	75.6	409	6	US-10-503-590A-2	Sequence 2, Appli
2	948	74.3	241	6	US-10-902-546-6	Sequence 6, Appli
3	936	73.4	241	6	US-10-902-546-5	Sequence 5, Appli
4	907	71.1	290	7	US-11-032-773-957	Sequence 957, App
5	907	71.1	319	7	US-11-032-773-955	Sequence 955, App
6	895	70.1	248	6	US-10-512-184-36	Sequence 36, Appl
7	895	70.1	615	6	US-10-512-184-50	Sequence 50, Appl
8	837.5	65.6	543	6	US-10-495-664-3	Sequence 3, Appli
9	832	65.2	237	6	US-10-073-301A-9	Sequence 9, Appli
10	832	65.2	237	7	US-11-203-137-9	Sequence 9, Appli
11	827	64.8	251	7	US-11-054-515-1921	Sequence 1921, Ap
12	827	64.8	251	7	US-11-266-444-1921	Sequence 1921, Ap
13	824.5	64.6	248	7	US-11-054-515-1778	Sequence 1778, Ap
14	824.5	64.6	248	7	US-11-266-444-1778	Sequence 1778, Ap
15	823	64.5	243	6	US-10-537-061-2	Sequence 2, Appli
16	822.5	64.5	250	7	US-11-054-515-932	Sequence 932, App
17	822.5	64.5	250	7	US-11-266-444-932	Sequence 932, App
18	821.5	64.4	248	7	US-11-054-515-1008	Sequence 1008, Ap
19	821.5	64.4	248	7	US-11-266-444-1008	Sequence 1008, Ap
20	819	64.2	245	7	US-11-054-515-1902	Sequence 1902, Ap
21	819	64.2	245	7	US-11-266-444-1902	Sequence 1902, Ap
22	815	63.9	243	7	US-11-054-515-2063	Sequence 2063, Ap
23	815	63.9	243	7	US-11-266-444-2063	Sequence 2063, Ap
24	813.5	63.8	248	7	US-11-054-515-1446	Sequence 1446, Ap
25	813.5	63.8	248	7	US-11-266-444-1446	Sequence 1446, Ap
26	809	63.4	243	6	US-10-537-061-3	Sequence 3, Appli
27	808.5	63.4	248	7	US-11-054-515-1104	Sequence 1104, Ap
28	808.5	63.4	248	7	US-11-266-444-1104	Sequence 1104, Ap
29	808	63.3	241	7	US-11-054-515-1948	Sequence 1948, Ap
30	808	63.3	241	7	US-11-266-444-1948	Sequence 1948, Ap
31	808	63.3	249	7	US-11-054-515-926	Sequence 926, App
32	808	63.3	249	7	US-11-266-444-926	Sequence 926, App
33	808	63.3	277	7	US-11-126-817-54	Sequence 54, Appl
34	804.5	63.0	248	7	US-11-054-515-1771	Sequence 1771, Ap
35	804.5	63.0	248	7	US-11-266-444-1771	Sequence 1771, Ap
36	804	63.0	249	7	US-11-054-515-918	Sequence 918, App
37	804	63.0	249	7	US-11-266-444-918	Sequence 918, App
38	803.5	63.0	248	7	US-11-054-515-1700	Sequence 1700, Ap
39	803.5	63.0	248	7	US-11-266-444-1700	Sequence 1700, Ap
40	803	62.9	249	7	US-11-054-515-919	Sequence 919, App
41	803	62.9	249	7	US-11-266-444-919	Sequence 919, App
42	801	62.8	249	7	US-11-054-515-1635	Sequence 1635, Ap
43	801	62.8	249	7	US-11-266-444-1635	Sequence 1635, Ap
44	800.5	62.7	246	7	US-11-054-515-2062	Sequence 2062, Ap
45	800.5	62.7	246	7	US-11-266-444-2062	Sequence 2062, Ap

ALIGNMENTS

RESULT 1
US-10-503-590A-2
; Sequence 2, Application US/10503590A
; Publication No. US20060062780A1
; GENERAL INFORMATION:
; APPLICANT: ZOCHER, MARCEL
; APPLICANT: DREIER, TORSTEN
; APPLICANT: BAEUERLE, PATRICK
; TITLE OF INVENTION: DE-IMMUNIZED (POLY)PEPTIDE CONSTRUCTS
; FILE REFERENCE: 028622-0134
; CURRENT APPLICATION NUMBER: US/10/503,590A
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: PCT/EP03/01389
; PRIOR FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: EP 02003332.0
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-590A-2

Query Match 75.6%; Score 964.5; DB 6; Length 409;
Best Local Similarity 77.3%; Pred. No. 1.5e-56;
Matches 187; Conservative 17; Mismatches 35; Indels 3; Gaps 1;

```
Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::||||| || :||||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db        162 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 221

Qy         63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS-- 120
              |||: ||||| ||||||||| | ||||||||||:|||   |    ||||||||:||||
Db        222 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSSVE 281

Qy        121 -GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPK 179
               | ||||| |  ||  ||:||||||||||||||||||| |||||||||:|||||||||
Db        282 GGSGGSGGGSGGSGGVDDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPK 341

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
              ||||||||:||||| |||||||| ||||||||:|||| |||||||||  ||||||||||
Db        342 RWIYDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 401

Qy        240 IK 241
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Db        402 LK 403
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RESULT 2
US-10-902-546-6
; Sequence 6, Application US/10902546
; Publication No. US20060024667A1
; GENERAL INFORMATION:
;  APPLICANT: Manucharyan, Karen
;  APPLICANT:  Gevorgyan, Gohar
;  TITLE OF INVENTION: CIP:  Compositions and Methods for Alzheimer's Disease
;  FILE REFERENCE: new
;  CURRENT APPLICATION NUMBER: US/10/902,546
;  CURRENT FILING DATE:  2004-07-29
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Peptide
US-10-902-546-6

  Query Match             74.3%;  Score 948;  DB 6;  Length 241;
  Best Local Similarity   75.0%;  Pred. No. 1.1e-55;
  Matches  180;  Conservative   25;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||| | |: |||||||||||||||| || | ::||:|:  : ||||| | |  |:: |
Db          1 QVKLQQWGTEVVKPGASVKLSCKASGYIFTSYDIDWVRQTPEQGLEWIGWIFPGEGSTEY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              |:||:|:|||:||||||||||:|  |||||||||||||| |  | || ||||||||||||
Db         61 NEKFKGRATLSVDKSSSTAYMELTRLTSEDSAVYFCARGDYYRRYFDLWGQGTTVTVSSC 120

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              ||||||||||||||||||||||||||||||:|||||||||: |::||||| |:||:
Db        121 GGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRLL 180

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              ||||| :| ||| |||||||| ||||||: :|||| ||||||:||||| ||| |||||:|
Db        181 IYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKLELK 240


RESULT 3
US-10-902-546-5
; Sequence 5, Application US/10902546
; Publication No. US20060024667A1
; GENERAL INFORMATION:
;  APPLICANT: Manucharyan, Karen
;  APPLICANT:  Gevorgyan, Gohar
;  TITLE OF INVENTION: CIP:  Compositions and Methods for Alzheimer's Disease
;  FILE REFERENCE: new
;  CURRENT APPLICATION NUMBER: US/10/902,546
;  CURRENT FILING DATE:  2004-07-29
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Peptide
US-10-902-546-5

  Query Match             73.4%;  Score 936;  DB 6;  Length 241;
  Best Local Similarity   73.8%;  Pred. No. 6.9e-55;
  Matches  177;  Conservative   27;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|| |: |||||||||||||||| || | ::||:|:  : ||||| | |  |:: :
Db          1 QVKLQESGTEVVKPGASVKLSCKASGYIFTSYDIDWVRQTPEQGLEWIGWIFPGEGSTEF 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              |:||:|:|||:||||||||||:|  |||||||||||||| |  | || ||||||||||||
Db         61 NEKFKGRATLSVDKSSSTAYMELTRLTSEDSAVYFCARGDYYRRYFDLWGQGTTVTVSSC 120

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              ||||||||||||||||||||||||||||||:|||||||||: |::||||| |:||:
Db        121 GGGSGGGGSGGGGSDIELTQSPTIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRLL 180

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              ||||| :| ||| |||||||| ||||||: :|||| ||||||:||||| ||| |||||:|
Db        181 IYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKLELK 240


RESULT 4
US-11-032-773-957
; Sequence 957, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
;  APPLICANT: Ault-Riche, Dana
;  APPLICANT:  Levy, Ronald
;  TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
;  FILE REFERENCE: 17102-013001 / 1762
;  CURRENT APPLICATION NUMBER: US/11/032,773
;  CURRENT FILING DATE:  2005-01-11
;  PRIOR APPLICATION NUMBER: 60/536,184
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: 60/557,591
;  PRIOR FILING DATE: 2004-03-29
;  NUMBER OF SEQ ID NOS: 958
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 957
;   LENGTH: 290
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pBAD S1C5 V5 His protein sequence
US-11-032-773-957

  Query Match             71.1%;  Score 907;  DB 7;  Length 290;
  Best Local Similarity   73.8%;  Pred. No. 6.4e-53;
  Matches  183;  Conservative   17;  Mismatches   40;  Indels    8;  Gaps    3;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|||||| || |||||||:|||||||:|| : ::||||   : |||||  |:| ||   |
Db          3 EVQLQQSGAELVKPGASVKISCKASGYTFTDHVIHWVKQRPEQGLEWIGFISPGNGDIRY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG--GYDGRGFDYWGQGTTVTVS 119
              |:||: ||||| |||||||||| |  ||||||||||||  |    ||    ||||||||:|||
Db         63 NEKFKDKATLTADKSSSTAYMQLNSLTSEDSAVYFCKRSFYYYDDNYGDYWGQGTTLTVS 122

Qy        120 S----GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV--SYMHWYQQK 173
              |    | |||||||||||||| ||||||||||  |:|||||:|||||  || ||||||
Db        123 SSGAPGGGGSGGGGSGGGGSDIVLTQSPAIMSASLEERVTMTCTASSSVSSSYFHWYQQK 182

Qy        174 SGTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFG 233
              |:||| ||| || |||||| |||||||| ||||||||:|||| |||||  |:   |||||
Db        183 PGSSPKLWIYTTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQYHRSPLTFG 242

Qy        234 AGTKLEIK 241
              ||||||:|
Db        243 AGTKLELK 250


RESULT 5
US-11-032-773-955
; Sequence 955, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
;  APPLICANT: Ault-Riche, Dana
;  APPLICANT:  Levy, Ronald
;  TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
;  FILE REFERENCE: 17102-013001 / 1762
;  CURRENT APPLICATION NUMBER: US/11/032,773
;  CURRENT FILING DATE:  2005-01-11
```

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;  PRIOR APPLICATION NUMBER: 60/536,184
;  PRIOR FILING DATE: 2004-01-12
;  PRIOR APPLICATION NUMBER: 60/557,591
;  PRIOR FILING DATE: 2004-03-29
;  NUMBER OF SEQ ID NOS: 958
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 955
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pBAD S1C5 CD20 His Protein Sequence
US-11-032-773-955

  Query Match             71.1%;  Score 907;  DB 7;  Length 319;
  Best Local Similarity   73.8%;  Pred. No. 6.9e-53;
  Matches  183;  Conservative   17;  Mismatches   40;  Indels    8;  Gaps    3;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :||||||| || |||||||:|||||||:|| : ::|||| : |||||  |:| ||   |
Db          3 EVQLQQSGAELVKPGASVKISCKASGYTFTDHVIHWVKQRPEQGLEWIGFISPGNGDIRY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG--GYDGRGFDYWGQGTTVTVS 119
              |:||: ||||| |||||||||| | |||||||||||| |    ||    ||||||||:|||
Db         63 NEKFKDKATLTADKSSSTAYMQLNSLTSEDSAVYFCKRSFYYYDDNYGDYWGQGTTLTVS 122

Qy        120 S----GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV--SYMHWYQQK 173
              |    | |||||||||||||| ||||||||||  |:|||||:|||||  || ||||||
Db        123 SSGAPGGGGSGGGGSGGGGSDIVLTQSPAIMSASLEERVTMTCTASSSVSSSYFHWYQQK 182

Qy        174 SGTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFG 233
              |:||| ||| || |||||| |||||||| ||||||||:|||| ||||| |:   |||||
Db        183 PGSSPKLWIYTTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQYHRSPLTFG 242

Qy        234 AGTKLEIK 241
              |||||||:|
Db        243 AGTKLELK 250


RESULT 6
US-10-512-184-36
; Sequence 36, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
;  APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
;  TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
;  TITLE OF INVENTION:  antibody fragments and fusions mediated plant disease
;  TITLE OF INVENTION:  resistance against fungi
;  FILE REFERENCE: 3581.01US01
;  CURRENT APPLICATION NUMBER: US/10/512,184
;  CURRENT FILING DATE:  2004-10-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: scFv SS2 with
;   OTHER INFORMATION: specificity against Sclerotinia sclerotiorum;
;   OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

  Query Match             70.1%;  Score 895;  DB 6;  Length 248;
  Best Local Similarity   73.1%;  Pred. No. 3.4e-52;
  Matches  179;  Conservative   20;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||||||||  | :||||||:|||||||:|| | |:|||| |: |||||  | | |  :||
Db          3 QVQLQQSGTVLARPGASVKMSCKASGYTFTSYWMHWVKQRPGQGLEWIGAIYPGNSDTSY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              ||||:||| ||   |:||||:| |||:||||||:| |  :|    |||||||:||||||
Db         63 NQKFKGKAKLTAVTSTSTAYMELSSLTNEDSAVYYCTRTDWD-YAMDYWGQGTSVTVSSG 121

Qy        122 -VGGSG----GGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGT 176
               |||     | ||   |  || | ||| |||||||||||||||||:|::||| ||||
Db        122 STSGSGKPGPGEGSTKGAPDIVLFQSPVIMSASPGEKVTMTCSASSSVNYIYWYQWKSGT 181

Qy        177 SPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGT 236
              ||||||:|||||||||| |||||||| |:||||||:|||| |||||||||  ||||||||
Db        182 SPKRWIFDTSKLASGVPVRFSGSGSGTSFSLTISSMEAEDIATYYCQQWSSPPLTFGAGT 241

Qy        237 KLEIK 241
              |||:|
Db        242 KLELK 246


RESULT 7
US-10-512-184-50
; Sequence 50, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
;  APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
;  TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
;  TITLE OF INVENTION:  antibody fragments and fusions mediated plant disease
;  TITLE OF INVENTION:  resistance against fungi
;  FILE REFERENCE: 3581.01US01
;  CURRENT APPLICATION NUMBER: US/10/512,184
;  CURRENT FILING DATE:  2004-10-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
;   LENGTH: 615
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: fusion protein
;   OTHER INFORMATION: comprising the leader peptide - chitinase - linker
;   OTHER INFORMATION: - scFv SS2 - cmyc/His6.
US-10-512-184-50

  Query Match             70.1%;  Score 895;  DB 6;  Length 615;
  Best Local Similarity   73.1%;  Pred. No. 7.4e-52;
  Matches  179;  Conservative   20;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||||||||  | :||||||:|||||||:|| | |:|||| |: |||||  | | |  :||
Db        344 QVQLQQSGTVLARPGASVKMSCKASGYTFTSYWMHWVKQRPGQGLEWIGAIYPGNSDTSY 403

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              ||||:||| ||   |:||||:| |||:||||||:| |  :|    |||||||:||||||
Db        404 NQKFKGKAKLTAVTSTSTAYMELSSLTNEDSAVYYCTRTDWD-YAMDYWGQGTSVTVSSG 462

Qy        122 -VGGSG----GGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGT 176
               |||     | ||   |  || | ||| |||||||||||||||||:|::||| ||||
Db        463 STSGSGKPGPGEGSTKGAPDIVLFQSPVIMSASPGEKVTMTCSASSSVNYIYWYQWKSGT 522

Qy        177 SPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGT 236
              ||||||:|||||||||| |||||||| |:||||||:|||| |||||||||  ||||||||
Db        523 SPKRWIFDTSKLASGVPVRFSGSGSGTSFSLTISSMEAEDIATYYCQQWSSPPLTFGAGT 582

Qy        237 KLEIK 241
              |||:|
Db        583 KLELK 587


RESULT 8
US-10-495-664-3
; Sequence 3, Application US/10495664
; Publication No. US20050244416A1
; GENERAL INFORMATION:
;  APPLICANT: JUNG, GUNDRAM
;  TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE
;  FILE REFERENCE: 034258-0801
;  CURRENT APPLICATION NUMBER: US/10/495,664
```

; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: PCT/EP02/12545
; PRIOR FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: DE 101 56 482.1
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: protein construct
US-10-495-664-3

Query Match 65.6%; Score 837.5; DB 6; Length 543;
Best Local Similarity 67.6%; Pred. No. 3.9e-48;
Matches 169; Conservative 22; Mismatches 46; Indels 13; Gaps 3;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:|||||||| |||||||:|||||||:|:   ||||||  |: ||||| | | :| ::|
Db        287 QVKLQQSGPELVKPGASVKISCKASGYAFSRSWMNWVKQRPGQGLEWIGRIYPGDGDTNY 346

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGG-----YDGRGFDYWGQGTTV 116
              | ||:|||||| |||||||||| : |||| ||||||||||      |     |||||||||
Db        347 NGKFKGKATLTADKSSSTAYMQVSSLTSVDSAVYFCARGNTVVVPYT---MDYWGQGTTV 403

Qy        117 TVSSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-----SYMHWYQ 171
              ||||| |||||||||||||||||||| :: | |:: |::| || ||      |:|||||
Db        404 TVSSGGGGSGGGGSGGGGSDIELTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQ 463

Qy        172 QKSGTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLT 231
              || |  ||  ||  | | |||| |||||||   ::|||  |||:| |||||||  :  |||
Db        464 QKPGQPPKLLIYLASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPLT 523

Qy        232 FGAGTKLEIK 241
              || |||||:|
Db        524 FGGGTKLELK 533
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RESULT 9
US-10-073-301A-9
; Sequence 9, Application US/10073301A
; Publication No. US20050255101A1
; GENERAL INFORMATION:
; APPLICANT: Reiter , Yoram
; APPLICANT: Denkberg, Galit
; TITLE OF INVENTION: ANTIBODY HAVING A T-CELL RECEPTOR-LIKE SPECIFICITY, YET HIGHER AF
; TITLE OF INVENTION: AND THE USE OF SAME IN THE DETECTION AND TREATMENT OF CANCER, VI
; TITLE OF INVENTION: AND AUTOIMMUNE DISEASE
; FILE REFERENCE: 01/23094
; CURRENT APPLICATION NUMBER: US/10/073,301A
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G1 single chain Fv- recombinant antibody protein sequence
US-10-073-301A-9

Query Match 65.2%; Score 832; DB 6; Length 237;
Best Local Similarity 65.0%; Pred. No. 4.4e-48;
Matches 154; Conservative 36; Mismatches 47; Indels 0; Gaps 0;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:||  | ||| |:|||| |||::|: | |:||:|:  | |||:  |:     : |
Db          1 QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
```

```
                :|: |:: | : :| |: : || |||:|:|:|||| ::|  || ||||||||||||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG 120

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              |||||||||||||:||||||||||||||||:||||||||| |::||||| |:||:
Db        121 GGGSGGGGSGGGGSNIELTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRLL 180

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
              ||||| :| ||| |||||||| |||||| :|||| ||||||:||||| ||| ||||
Db        181 IYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL 237
```

RESULT 10
US-11-203-137-9
; Sequence 9, Application US/11203137
; Publication No. US20050287141A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Denkberg, Galit
; TITLE OF INVENTION: ANTIBODY HAVING A T-CELL RECEPTOR-LIKE SPECIFICITY, YET HIGHER A
; TITLE OF INVENTION: AND THE USE OF SAME IN THE DETECTION AND TREATMENT OF CANCER, V
; TITLE OF INVENTION: AND AUTOIMMUNE DISEASE
; FILE REFERENCE: 30177
; CURRENT APPLICATION NUMBER: US/11/203,137
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G1 single chain Fv- recombinant antibody protein sequence
US-11-203-137-9

Query Match 65.2%; Score 832; DB 7; Length 237;
Best Local Similarity 65.0%; Pred. No. 4.4e-48;
Matches 154; Conservative 36; Mismatches 47; Indels 0; Gaps 0;

```
Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:||  | ||| |:|||| |||::|: | |:||:|:  | |||:  |:     : |
Db          1 QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
                :|: |:: | : :| |: : || |||:|:|:|||| ::|  || ||||||||||||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG 120

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              |||||||||||||:||||||||||||||||:||||||||| |::||||| |:||:
Db        121 GGGSGGGGSGGGGSNIELTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRLL 180

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKL 238
              ||||| :| ||| |||||||| |||||| :|||| ||||||:||||| ||| ||||
Db        181 IYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL 237
```

RESULT 11
US-11-054-515-1921
; Sequence 1921, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469

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;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1921
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1921

  Query Match             64.8%;  Score 827;  DB 7;  Length 251;
  Best Local Similarity   63.2%;  Pred. No. 9.8e-48;
  Matches  158;  Conservative   37;  Mismatches   45;  Indels   10;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              |||| ||| |::|||||||:|||||||:|| | ::||:|: |: |||:| |: ||| ::|
Db          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCAR---------GGYDGRGFDYWGQ 112
                || :|: |:| | |:|||||:| || |:|:|||:|||         |||   | | ||:
Db         61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVTSLYSSSSGGYYYYGMDVWGR 120

Qy        113 GTTVTVSSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-SYMHWYQ 171
              ||||||||| |||||||||||||||::||||: :||| |::||:|| ||  : :|: |||
Db        121 GTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSFLSASVGDRVTITCRASQGINNYLAWYQ 180

Qy        172 QKSGTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLT 231
              || | :||  ||  | | |||| |||||||  ::|||||:: || |||| | | ||||
Db        181 QKPGRAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQDSDYPLT 240

Qy        232 FGAGTKLEIK 241
              || |||||||
Db        241 FGGGTKLEIK 250


RESULT 12
US-11-266-444-1921
; Sequence 1921, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato
;  FILE REFERENCE: PF523P1D1
;  CURRENT APPLICATION NUMBER: US/11/266,444
;  CURRENT FILING DATE:  2005-11-04
;  PRIOR APPLICATION NUMBER: 09/880,746
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1921
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-266-444-1921

  Query Match             64.8%;  Score 827;  DB 7;  Length 251;
  Best Local Similarity   63.2%;  Pred. No. 9.8e-48;
  Matches  158;  Conservative   37;  Mismatches   45;  Indels   10;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              |||| ||| |::|||||||:|||||||:|| | ::||:|: |: |||:| |: ||| ::|
Db          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCAR---------GGYDGRGFDYWGQ 112
                || :|: |:| | |:|||||:| || |:|:|||:|||         |||   | | ||:
Db         61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVTSLYSSSSGGYYYYGMDVWGR 120

Qy        113 GTTVTVSSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-SYMHWYQ 171
              ||||||||| |||||||||||||||::||||: :||| |::||:|| ||  : :|: |||
Db        121 GTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSFLSASVGDRVTITCRASQGINNYLAWYQ 180

Qy        172 QKSGTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLT 231
              || | :||  ||  | | |||| |||||||  ::|||||:: || |||| | | ||||
Db        181 QKPGRAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQDSDYPLT 240

Qy        232 FGAGTKLEIK 241
              || |||||||
Db        241 FGGGTKLEIK 250


RESULT 13
US-11-054-515-1778
; Sequence 1778, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1778
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1778

  Query Match             64.6%;  Score 824.5;  DB 7;  Length 248;
  Best Local Similarity   63.2%;  Pred. No. 1.4e-47;
  Matches  156;  Conservative   37;  Mismatches   47;  Indels    7;  Gaps    2;

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Db          1 QVQLQQSGAEVRKPGASVKVSCKASGYTFTSYGISWVRQAPGHGLEWMGWISAYNGNTNY 60
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               || :|: |:| | |:|||||:| || |:|:|||:|||        ||    | | ||:||
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Qy         116 VTVSSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-SYMHWYQQKS 174
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Db         121 VTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQQKP 180

Qy         175 GTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGA 234
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Qy         235 GTKLEIK 241
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Db         241 GTKLEIK 247
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RESULT 14
US-11-266-444-1778
; Sequence 1778, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1778
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1778

Query Match 64.6%; Score 824.5; DB 7; Length 248;
Best Local Similarity 63.2%; Pred. No. 1.4e-47;
Matches 156; Conservative 37; Mismatches 47; Indels 7; Gaps 2;

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               |||||||| |: |||||||:|||||||:|| | ::||:|: |  |||:| |: ||| ::|
Db           1 QVQLQQSGAEVRKPGASVKVSCKASGYTFTSYGISWVRQAPGHGLEWMGWISAYNGNTNY 60

Qy          62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG------GYDGRGFDYWGQGTT 115
               || :|: |:| | |:|||||:| || |:|:|||:|||        ||    | | ||:||
Db          61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARSYYDILTGYYPFGMDVWGKGTM 120

Qy         116 VTVSSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSV-SYMHWYQQKS 174
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Db         121 VTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQQKP 180

Qy         175 GTSPKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGA 234
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Db         241 GTKLEIK 247
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RESULT 15
US-10-537-061-2
; Sequence 2, Application US/10537061
; Publication No. US20060051359A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
; APPLICANT: Pastan, Ira
; APPLICANT: Onda, Masanori
; APPLICANT: Cheung, Nai-Kong
; TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9
; TITLE OF INVENTION: (FV)-PE38 AGAINST BREAST CANCER, OSTEOCARCINOMA AND NEUROBLASTC
; FILE REFERENCE: 4239-67287-05
; CURRENT APPLICATION NUMBER: US/10/537,061
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: PCT/US03/038227
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/430,305
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-537-061-2

Query Match 64.5%; Score 823; DB 6; Length 243;
Best Local Similarity 66.4%; Pred. No. 1.7e-47;
Matches 160; Conservative 29; Mismatches 50; Indels 2; Gaps 2;

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               ||:||||| || |||||||||||||||:|| | :|||:|   : ||||| | | :|:: |
Db           1 QVKLQQSGAELVKPGASVKLSCKASGYTFTNYDINWVRQRPEQGLEWIGWIFPGDGSTQY 60

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Db          61 NEKFKGKATLTTDTSSSTAYMQLSRLTSEDSAVYFCAR-QTTATWFAYWGQGTTVTVSSD 119

Qy         122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVS-YMHWYQQKSGTSPKR 180
               ||||||||||||||||||||  :| :||::|:::| || |:| |:|||||||  ||:
Db         120 GGGSGGGGSGGGGSDIELTQSPTTLSVTPGDRVSLSCRASQSISDYLHWYQQKSHESPRL 179

Qy         181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
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Qy         241 K 241
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Db         240 K 240
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Job time : 46 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 3, 2006, 05:30:14 ; Search time 23 Seconds
(without alignments)
866.297 Million cell updates/sec

Title: US-09-979-539-1
Perfect score: 1276
Sequence: 1 MQVQLQQSGPELEKPGASVK.....CQQWSGYPLTFGAGTKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1274	99.8	241	2	US-09-581-345-5	Sequence 5, Appli
2	1010.5	79.2	239	2	US-09-830-954A-6	Sequence 6, Appli
3	993	77.8	244	1	US-08-553-497A-20	Sequence 20, Appl
4	987	77.4	242	1	US-08-553-497A-26	Sequence 26, Appl
5	982.5	77.0	297	2	US-09-486-814A-2	Sequence 2, Appli
6	981.5	76.9	599	1	US-08-463-163-3	Sequence 3, Appli
7	979	76.7	244	1	US-08-553-497A-22	Sequence 22, Appl
8	977	76.6	242	1	US-08-553-497A-28	Sequence 28, Appl
9	976.5	76.5	239	2	US-08-279-772A-8	Sequence 8, Appli
10	976.5	76.5	239	2	US-08-902-486-11	Sequence 11, Appl
11	972	76.2	246	1	US-08-553-497A-24	Sequence 24, Appl
12	959.5	75.2	256	2	US-09-526-738A-2	Sequence 2, Appli
13	959.5	75.2	258	2	US-09-526-738A-4	Sequence 4, Appli
14	956.5	75.0	495	2	US-09-948-004-18	Sequence 18, Appl
15	908	71.2	238	2	US-09-798-689-21	Sequence 21, Appl
16	902.5	70.7	246	1	US-08-469-486-57	Sequence 57, Appl
17	902.5	70.7	246	1	US-08-469-658-57	Sequence 57, Appl
18	897.5	70.3	264	2	US-10-114-716A-46	Sequence 46, Appl
19	889.5	69.7	270	1	US-08-652-507-2	Sequence 2, Appli
20	885.5	69.4	281	2	US-09-423-439-44	Sequence 44, Appl
21	885.5	69.4	666	2	US-09-423-439-51	Sequence 51, Appl
22	883.5	69.2	553	1	US-08-661-052-16	Sequence 16, Appl
23	883.5	69.2	553	2	US-09-188-082-16	Sequence 16, Appl
24	883.5	69.2	553	2	US-09-364-088-16	Sequence 16, Appl
25	883.5	69.2	553	2	US-09-102-716-16	Sequence 16, Appl
26	866	67.9	267	2	US-09-485-737B-2	Sequence 2, Appli
27	866	67.9	267	2	US-10-071-485-2	Sequence 2, Appli
28	866	67.9	541	2	US-09-485-737B-85	Sequence 85, Appl
29	866	67.9	541	2	US-10-071-485-85	Sequence 85, Appl
30	866	67.9	711	2	US-09-485-737B-90	Sequence 90, Appl
31	866	67.9	711	2	US-10-071-485-90	Sequence 90, Appl
32	854	66.9	284	2	US-09-184-658-40	Sequence 40, Appl
33	854	66.9	284	2	US-09-504-262D-40	Sequence 40, Appl
34	849.5	66.6	255	2	US-09-553-498-8	Sequence 8, Appli
35	849.5	66.6	255	2	US-09-618-869-8	Sequence 8, Appli
36	841.5	65.9	273	1	US-08-403-853-18	Sequence 18, Appl
37	841	65.9	235	1	US-08-190-199A-61	Sequence 61, Appl
38	839	65.8	267	2	US-09-419-788-30	Sequence 30, Appl
39	834.5	65.4	240	2	US-09-485-737B-91	Sequence 91, Appl
40	834.5	65.4	240	2	US-10-071-485-91	Sequence 91, Appl
41	831.5	65.2	240	1	US-08-800-198-8	Sequence 8, Appli
42	831.5	65.2	240	2	US-09-296-595-8	Sequence 8, Appli
43	829	65.0	288	2	US-09-423-439-38	Sequence 38, Appl
44	829	65.0	673	2	US-09-423-439-32	Sequence 32, Appl
45	823	64.5	260	1	US-08-447-402-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-581-345-5
; Sequence 5, Application US/09581345
; Patent No. 6809184
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; APPLICANT: Chowdhury, Partha S.
; APPLICANT: The Government of the United States
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Antibodies, Including Fv Molecules, and
; TITLE OF INVENTION: Immunoconjugates Having High Binding Affinity for
; TITLE OF INVENTION: Mesothelin and Methods for Their Use
; FILE REFERENCE: 015280-339100US
; CURRENT APPLICATION NUMBER: US/09/581,345
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/067,175
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: WO PCT/US98/25270
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SS scFv
US-09-581-345-5

Query Match 99.8%; Score 1274; DB 2; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.3e-95;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MQVQLQQSGPELEKPGASVKISCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASS 60

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Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
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Db        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
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Qy        241 K 241
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Db        241 K 241


RESULT 2
US-09-830-954A-6
; Sequence 6, Application US/09830954A
; Patent No. 6919075
; GENERAL INFORMATION:
;  APPLICANT: SOLOMON, Beka
;  APPLICANT:  FRENKEL, Dan
;  APPLICANT:  HANAN, Eilat
;  TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
;  TITLE OF INVENTION:  AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
;  FILE REFERENCE: SOLOMON=2C
;  CURRENT APPLICATION NUMBER: US/09/830,954A
;  CURRENT FILING DATE:  2001-05-03
;  PRIOR APPLICATION NUMBER: PCT/IL00/00518
;  PRIOR FILING DATE: 2000-08-31
;  PRIOR APPLICATION NUMBER: 09/629,971
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/473,653
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: US 60/152,417
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-830-954A-6

  Query Match             79.2%;  Score 1010.5;  DB 2;  Length 239;
  Best Local Similarity   79.8%;  Pred. No. 2.8e-74;
  Matches  194;  Conservative   16;  Mismatches   26;  Indels    7;  Gaps    2;

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Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG---GYDGRGFDYWGQGTTVTV 118
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Db         61 NQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARGATMSY----FDYWGQVTTVTV 116

Qy        119 SSGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP 178
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Db        237 EIK 239


RESULT 3
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
;  GENERAL INFORMATION:
;    APPLICANT:  KETTLEBOROUGH, C. A.
;    APPLICANT:  BENDIG, MARY M.
;    APPLICANT:  ANSELL, KEITH H.
;    APPLICANT:  GUSSOW, DETLEF
;    APPLICANT:  ADAN, JAUME
;    APPLICANT:  MITJANS, FRANSESC
;    APPLICANT:  ROSELL, ELISABET
;    APPLICANT:  BLASCO, FRANCESC
;    APPLICANT:  PIULATS, JAUME
;    TITLE OF INVENTION:  ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BLVD. SUITE 1400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,497A
;      FILING DATE:  17-NOV-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP95/00978
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94104160.0
;      FILING DATE:  17-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94118970.6
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAMLET-KING, DIANA
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  MERCK 1726
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  244 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-553-497A-20

  Query Match             77.8%;  Score 993;  DB 1;  Length 244;
  Best Local Similarity   79.9%;  Pred. No. 7.4e-73;
  Matches  195;  Conservative   14;  Mismatches   31;  Indels    4;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
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Qy        120 SGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPK 179
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Db        121 SGGGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMYWYQQKPGSSPR 180

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYP--LTFGAGTK 237
                |||||| |||||| |||||||| ||||||| :|||| ||||||||| ||   ||| |||
Db        181 LLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPPMYTFGGGTK 240

Qy        238 LEIK 241
              ||||
Db        241 LEIK 244


RESULT 4
US-08-553-497A-26
; Sequence 26, Application US/08553497A
; Patent No. 5844093
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  KETTLEBOROUGH, C. A.
;    APPLICANT:  BENDIG, MARY M.
;    APPLICANT:  ANSELL, KEITH H.
;    APPLICANT:  GUSSOW, DETLEF
;    APPLICANT:  ADAN, JAUME
;    APPLICANT:  MITJANS, FRANSESC
;    APPLICANT:  ROSELL, ELISABET
;    APPLICANT:  BLASCO, FRANCESC
;    APPLICANT:  PIULATS, JAUME
;    TITLE OF INVENTION:  ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BLVD. SUITE 1400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,497A
;      FILING DATE:  17-NOV-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP95/00978
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94104160.0
;      FILING DATE:  17-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94118970.6
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAMLET-KING, DIANA
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  MERCK 1726
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  242 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-553-497A-26

  Query Match             77.4%;  Score 987;  DB 1;  Length 242;
  Best Local Similarity   79.3%;  Pred. No. 2.2e-72;
  Matches  192;  Conservative   16;  Mismatches   32;  Indels    2;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|| || |||||||||||||||:|| : |:||||  |: ||||| | |    ::|
Db          1 QVKLQESGAELVKPGASVKLSCKASGYTFTSHWMHWVKQRAGQGLEWIGEINPRTAPTNY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG--GYDGRGFDYWGQGTTVTVS 119
              |:||: |||||||||||||| | ||||||||||:||     |||| ||||||||||||
Db         61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCASRDYDYDGRYFDYWGQGTTVTVS 120

Qy        120 SGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPK 179
              || |||||||||||||||||||| |||||||||||||| |||||| :|||||:|:||:
Db        121 SGGGGSGGGGSGGGGSDIELTQSPTIMSASPGEKVTMTCSDSSSVSYTYWYQQKTGSSPR 180

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
                |||||  |||||| |||||||| ||||||| :|||| |||||||| ||||||||||||
Db        181 LLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPLTFGAGTKLE 240

Qy        240 IK 241
              ||
Db        241 IK 242


RESULT 5
US-09-486-814A-2
; Sequence 2, Application US/09486814A
; Patent No. 6562599
; GENERAL INFORMATION:
;  APPLICANT: YAMAMOTO, Masato
;  APPLICANT:  HAYASHI, No. 6562599io
;  APPLICANT:  YAMAMOTO, Hiroko
;  APPLICANT:  TOHDOH, Naoki
;  TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
;  TITLE OF INVENTION:  PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
;  TITLE OF INVENTION:  HEPATITIS B CONTAINING THESE
;  FILE REFERENCE: 0020-4682P
;  CURRENT APPLICATION NUMBER: US/09/486,814A
;  CURRENT FILING DATE:  2002-06-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 297
;   TYPE: PRT
;   ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(145)
;   OTHER INFORMATION: Identification Method: P
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (177)..(279)
;   OTHER INFORMATION: Identification Method: P
US-09-486-814A-2

  Query Match             77.0%;  Score 982.5;  DB 2;  Length 297;
  Best Local Similarity   78.7%;  Pred. No. 6.6e-72;
  Matches  192;  Conservative   15;  Mismatches   28;  Indels    9;  Gaps    3;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||:|||||||||||||:|||||||||| | |||||:|||||||| | |||| : |
Db         40 QVKLQESGPELEKPGASVKISCKASGYSFTGYNMKWVKQSNGKSLEWIGYIYPYNGGTGY 99

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              ||||: |||||||||||||| | ||||||||||:|||      | ||||||||||||||
Db        100 NQKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR-----LGLDYWGQGTTVTVSSG 154

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVS--YMHWYQQKSGTSPK 179
              |||||||||||||||||||||  |:||||||:|:|||||||:|  |:|||||| | |||
Db        155 GGGSGGGGSGGGGSDIELTQSPTTMAASPGEKITITCSASSSISSNYLHWYQQKPGFSPK 214

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYP--LTFGAGTK 237
                || || ||||:| |||||||| |||||| ::|||| |||||||  |   |   |||||||
Db        215 LLIYRTSNLASGIPARFSGSGSGTSYSLTIGTMEAEDVATYYCQQGSSIPRIFTFGAGTK 274

Qy        238 LEIK 241
              ||||
Db        275 LEIK 278


RESULT 6
US-08-463-163-3
; Sequence 3, Application US/08463163
; Patent No. 5696237
;  GENERAL INFORMATION:
;    APPLICANT:  FitzGerald, David J.
;    APPLICANT:  Chaudhary, Vijay K.
;    APPLICANT:  Pastan, Ira H.
;    APPLICANT:  Waldmann, Thomas A.
;    APPLICANT:  Queen, Cary L.
;    TITLE OF INVENTION:  Recombinant Antibody-Toxin Fusion Protein
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
```

; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,163
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/227,227
; FILING DATE: 22-JAN-1981
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/911,227
; FILING DATE: 24-SEP-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,361
; FILING DATE: 21-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865,722
; FILING DATE: 08-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-12211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-163-3

Query Match 76.9%; Score 981.5; DB 1; Length 599;
Best Local Similarity 78.8%; Pred. No. 1.8e-71;
Matches 190; Conservative 14; Mismatches 34; Indels 3; Gaps 1;

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Qy          1 MQVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASS 60
              |||||||||  ||  |||||||:|||||||:||  |  |:||||   |: |||||  |  |   | :
Db          1 MQVQLQQSGAELAKPGASVKMSCKASGYTFTSYRMHWVKQRPGQGLEWIGYINPSTGYTE 60

Qy         61 YNQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS 120
              |||||: |||||  |||||||||  |  |||  ||||||:||||    |  ||||||||:||||
Db         61 YNQKFKDKATLTADKSSSTAYMQLSSLTFEDSAVYYCARG---GGVFDYWGQGTTLTVSS 117

Qy        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKR 180
              | ||||||||||||  |  ||||||||||||||||||:|||||||:|||||:|||  |||||
Db        118 GGGGSGGGGSGGGGSQIVLTQSPAIMSASPGEKVTITCSASSSISYMHWFQQKPGTSPKL 177

Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
              |||  ||  ||||||  ||||||||  |||||||  :||||  |||||  |  |  ||||||:|||||:
Db        178 WIYTTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCHQRSTYPLTFGSGTKLEL 237

Qy        241 K 241
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Db        238 K 238
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RESULT 7
US-08-553-497A-22
; Sequence 22, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANSESC
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-497A-22

Query Match 76.7%; Score 979; DB 1; Length 244;
Best Local Similarity 78.7%; Pred. No. 1e-71;
Matches 192; Conservative 15; Mismatches 33; Indels 4; Gaps 2;

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Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|||||| || ||||||||||||||:|| : |:||||  |: |||||   | || ::|
Db          1 EVQLQQSGAELVKPGASVKLSCKASGYTFTSHWMHWVKQRAGQGLEWIGEFNPSNGRTNY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG--GYDGRGFDYWGQGTTVTVS 119
              |:| : ||||||||||||||| | ||||||||||:||     ||||  ||||||||||||
Db         61 NEKIKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCASRDYDYDGRYFDYWGQGTTVTVS 120

Qy        120 SGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPK 179
              || |||||||||||||||||||| |||||||||||||| |||||||:|||||:|:||:
Db        121 SGGGGSGGGGSGGGGSDIELTQSPTIMSASPGEKVTMTCSDSSSVSYMYWYQQKTGSSPR 180

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYP--LTFGAGTK 237
                |||||  ||||||  ||||||||  |||||||  :||||  |||||||||  ||   |||  |||
Db        181 LLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPPMYTFGGGTK 240

Qy        238 LEIK 241
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Db        241 LEIK 244


RESULT 8
US-08-553-497A-28
; Sequence 28, Application US/08553497A
; Patent No. 5844093
;  GENERAL INFORMATION:
;    APPLICANT:  KETTLEBOROUGH, C. A.
;    APPLICANT:  BENDIG, MARY M.
;    APPLICANT:  ANSELL, KEITH H.
;    APPLICANT:  GUSSOW, DETLEF
;    APPLICANT:  ADAN, JAUME
;    APPLICANT:  MITJANS, FRANSESC
;    APPLICANT:  ROSELL, ELISABET
;    APPLICANT:  BLASCO, FRANCESC
;    APPLICANT:  PIULATS, JAUME
;    TITLE OF INVENTION:  ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BLVD. SUITE 1400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,497A
;      FILING DATE:  17-NOV-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP95/00978
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94104160.0
;      FILING DATE:  17-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94118970.6
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAMLET-KING, DIANA
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  MERCK 1726
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  242 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-553-497A-28

  Query Match             76.6%;  Score 977;  DB 1;  Length 242;
  Best Local Similarity   78.1%;  Pred. No. 1.4e-71;
  Matches  189;  Conservative   19;  Mismatches   32;  Indels    2;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|:||||| || ||||||||||||||:|| :  :|||   : |||||   | || ::|
Db          1 EVKLQQSGAELVKPGASVKLSCKASGYTFTSHLDHWVKQRGWQGLEWIGQFNPSNGRTNY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG--GYDGRGFDYWGQGTTVTVS 119
              |:||: |||||||||||||::| ||||||  :||:||     |||| ||||||||||||
Db         61 NEKFKSKATLTVDKSSSTAYIELSSLTSEDCSVYYCASRDYDYDGRYFDYWGQGTTVTVS 120

Qy        120 SGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPK 179
                || |||||||||||||||||||| |||||||||||||| ||||||:|||||:|:||:
Db        121 SGGGGSGGGGSGGGGSDIELTQSPTIMSASPGEKVTMTCSDSSSVSYMYWYQQKTGSSPR 180

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
                |||||  |||||| |||||||| |||||| :|||| |||||||| ||||||||||||
Db        181 LLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPLTFGAGTKLE 240

Qy        240 IK 241
              ||
Db        241 IK 242


RESULT 9
US-08-279-772A-8
; Sequence 8, Application US/08279772A
; Patent No. 6080560
;  GENERAL INFORMATION:
;    APPLICANT:  Russell, David R
;    APPLICANT:  Fuller, James T
;    TITLE OF INVENTION:  Method for Producing Antibodies in Plant
;    TITLE OF INVENTION:  Cells
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles and Brady
;      STREET:  PO Box 2113
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  United States of America
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/279,772A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27,386
;      REFERENCE/DOCKET NUMBER:  11-229-9097-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  239 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-279-772A-8

  Query Match             76.5%;  Score 976.5;  DB 2;  Length 239;
  Best Local Similarity   78.8%;  Pred. No. 1.6e-71;
  Matches  189;  Conservative   14;  Mismatches   34;  Indels    3;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              |||||||| || |||||||:|||||||:|| | |:||||  |: ||||| | |  | : |
Db          3 QVQLQQSGAELAKPGASVKMSCKASGYTFTSYRMHWVKQRPGQGLEWIGYINPSTGYTEY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              ||||: ||||| |||||||||| | ||| ||||||:||||    |  |||||||||:|||||
Db         63 NQKFKDKATLTADKSSSTAYMQLSSLTFEDSAVYYCARG---GGVFDYWGQGTTLTVSSG 119

Qy        122 VGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              |||||||||||||| | |||||||||||||||:|||||||:|||||:||| ||||| |
Db        120 GGGSGGGGSGGGGSQIVLTQSPAIMSASPGEKVTITCSASSSISYMHWFQQKPGTSPKLW 179

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              || || |||||| |||||||| ||||||| :|||| ||||| | | |||||||:|||||:|
Db        180 IYTTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCHQRSTYPLTFGSGTKLELK 239
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RESULT 10
US-08-902-486-11
; Sequence 11, Application US/08902486
; Patent No. 6140075
;  GENERAL INFORMATION:
;    APPLICANT:  Russel, David R.
;    APPLICANT:  Fuller, James T.
;    TITLE OF INVENTION:  METHOD FOR PRODUCING ANTIBODIES AND
;    TITLE OF INVENTION:  PROTEIN TOXINS IN PLANT CELLS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/902,486
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  670513.90261
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 239 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-902-486-11

  Query Match             76.5%;  Score 976.5;  DB 2;  Length 239;
  Best Local Similarity   78.8%;  Pred. No. 1.6e-71;
  Matches  189;  Conservative   14;  Mismatches   34;  Indels    3;  Gaps    1;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              |||||||| || |||||||:|||||||:|| | |:|||| |: ||||| | |  | : |
Db          3 QVQLQQSGAELAKPGASVKMSCKASGYTFTSYRMHWVKQRPGQGLEWIGYINPSTGYTEY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSSG 121
              ||||: ||||| |||||||||  | ||| ||||||:||||    |  |||||||||:|||||
Db         63 NQKFKDKATLTADKSSSTAYMQLSSLTFEDSAVYYCARG---GGVFDYWGQGTTLTVSSG 119

Qy        122 VGGSGGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRW 181
              |||||||||||||  | ||||||||||||||||||:|||||||:|||||:||| ||||| |
Db        120 GGGSGGGGGSGGGGSQIVLTQSPAIMSASPGEKVTITCSASSSISYMHWFQQKPGTSPKLW 179

Qy        182 IYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEIK 241
              || || |||||| |||||||| ||||||| :|||| ||||| | | ||||||:|||||:|
Db        180 IYTTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCHQRSTYPLTFGSGTKLELK 239


RESULT 11
US-08-553-497A-24
; Sequence 24, Application US/08553497A
; Patent No. 5844093
;  GENERAL INFORMATION:
;    APPLICANT:  KETTLEBOROUGH, C. A.
;    APPLICANT:  BENDIG, MARY M.
;    APPLICANT:  ANSELL, KEITH H.
;    APPLICANT:  GUSSOW, DETLEF
;    APPLICANT:  ADAN, JAUME
;    APPLICANT:  MITJANS, FRANSESC
;    APPLICANT:  ROSELL, ELISABET
;    APPLICANT:  BLASCO, FRANCESC
;    APPLICANT:  PIULATS, JAUME
;    TITLE OF INVENTION:  ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BLVD. SUITE 1400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,497A
;      FILING DATE:  17-NOV-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP95/00978
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94104160.0
;      FILING DATE:  17-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94118970.6
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAMLET-KING, DIANA
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  MERCK 1726
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-553-497A-24

  Query Match             76.2%;  Score 972;  DB 1;  Length 246;
  Best Local Similarity   78.5%;  Pred. No. 3.7e-71;
  Matches  193;  Conservative   14;  Mismatches   33;  Indels    6;  Gaps    3;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              :|||||| || |||||||||||||:|| : |:|||| |: |||||  | || ::|
Db          1 EVQLQQSGAELVKPGASVKLSCKASGYTFTSHWMHWVKQRAGQGLEWIGEFNPSNGRTNY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG--GYDGRGFDYWGQGTTVTVS 119
              |:||: |||||||||||||| | ||||||||||:||     |||| ||||||||||||||
Db         61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCASRDYDYDGRYFDYWGQGTTVTVS 120

Qy        120 SGVGGSGGGGSGGG--GSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTS 177
              || |||||||||  |||||||| |||||||||||||||| |||||||:||||| |:|
Db        121 SGGGGSGGGGSGGGGSGSDIELTQSPTIMSASPGEKVTMTCSDSSSVSYMYWYQQKPGSS 180

Qy        178 PKRWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYP--LTFGAG 235
              |:  ||||| |||||| |||||||| ||||||| :|||| |||||||| ||    ||| |
Db        181 PRLLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPPMYTFGGG 240

Qy        236 TKLEIK 241
              ||||||
Db        241 TKLEIK 246


RESULT 12
```

```
US-09-526-738A-2
; Sequence 2, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
;  APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DVELOPMENT
;  APPLICANT:  LTD.
;  TITLE OF INVENTION: SINGLE CHAIN  ANTIBODY AGAINST MUTANT P53
;  FILE REFERENCE: 1196336
;  CURRENT APPLICATION NUMBER: US/09/526,738A
;  CURRENT FILING DATE:  2000-03-16
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Hunanus
US-09-526-738A-2

  Query Match           75.2%;  Score 959.5;  DB 2;  Length 256;
  Best Local Similarity  77.6%;  Pred. No. 4e-70;
  Matches  187;  Conservative   13;  Mismatches   36;  Indels    5;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||||| || |||||||:||| |||:|| | ||||||  |: ||||| | |  | : |
Db          1 QVKLQQSGAELAKPGASVKMSCKTSGYTFTSYWMNWVKQRPGQGLEWIGYINPTTGYTKY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG-GYDGRGFDYWGQGTTVTVSS 120
              ||||: ||||| ||||||||| | |||: |||||:|  |  |    |||||||||||||
Db         61 NQKFKDKATLTADKSSSTAYMQLSSLTNVDSAVYYCTTGYSY----FDYWGQGTTVTVSS 116

Qy        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKR 180
              | ||||||||||||||||||||||||||||||:||||||||:||||:||| |||||
Db        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTITCSASSSVNYMHWFQQKPGTSPKL 176

Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
              ||  || |||||| |||||||| ||||||| :|||| ||||||| | || ||| ||||:|
Db        177 WISSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPYTFGGGTKLQI 236

Qy        241 K 241
              |
Db        237 K 237


RESULT 13
US-09-526-738A-4
; Sequence 4, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
;  APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DVELOPMENT
;  APPLICANT:  LTD.
;  TITLE OF INVENTION: SINGLE CHAIN  ANTIBODY AGAINST MUTANT P53
;  FILE REFERENCE: 1196336
;  CURRENT APPLICATION NUMBER: US/09/526,738A
;  CURRENT FILING DATE:  2000-03-16
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Humanus
US-09-526-738A-4

  Query Match           75.2%;  Score 959.5;  DB 2;  Length 258;
  Best Local Similarity  77.6%;  Pred. No. 4.1e-70;
  Matches  187;  Conservative   13;  Mismatches   36;  Indels    5;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||||| || |||||||:||| |||:|| | ||||||  |: ||||| | |  | : |
Db          3 QVKLQQSGAELAKPGASVKMSCKTSGYTFTSYWMNWVKQRPGQGLEWIGYINPTTGYTKY 62

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARG-GYDGRGFDYWGQGTTVTVSS 120
              ||||: ||||| ||||||||| | |||: |||||:|  |  |    |||||||||||||
Db         63 NQKFKDKATLTADKSSSTAYMQLSSLTNVDSAVYYCTTGYSY----FDYWGQGTTVTVSS 118

Qy        121 GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKR 180
              | ||||||||||||||||||||||||||||||:||||||||:||||:||| |||||
Db        119 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTITCSASSSVNYMHWFQQKPGTSPKL 178

Qy        181 WIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLEI 240
              ||  || |||||| |||||||| ||||||| :|||| ||||||| | || ||| ||||:|
Db        179 WISSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPYTFGGGTKLQI 238

Qy        241 K 241
              |
Db        239 K 239


RESULT 14
US-09-948-004-18
; Sequence 18, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
;  APPLICANT: MACK, Matthias
;  TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
;  TITLE OF INVENTION:  immunological disorders
;  FILE REFERENCE: E 2411 EP
;  CURRENT APPLICATION NUMBER: US/09/948,004
;  CURRENT FILING DATE:  2001-09-05
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 495
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-948-004-18

  Query Match           75.0%;  Score 956.5;  DB 2;  Length 495;
  Best Local Similarity  76.9%;  Pred. No. 1.5e-69;
  Matches  186;  Conservative   17;  Mismatches   36;  Indels    3;  Gaps    1;

Qy          3 VQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSYN 62
              ::|||||  || :||||||:||| |||:|| |||:|||| |: ||||| | |  | ::||
Db        248 IKLQQSGAELARPGASVKMSCKTSGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYN 307

Qy         63 QKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTTVTVSS-- 120
              |||: ||||| |||||||||| | ||||||||||:|||    |     ||| ||||:||||
Db        308 QKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWRQGTTLTVSSVE 367

Qy        121 -GVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPK 179
               | ||||| |  ||  ||:|||||||||||||||||| ||||||||:||||||||||
Db        368 GGSGGSGGGSGGSGGVDDIQLTQSPAIMSASPGEKVTMTCRASSSVSYMNWYQQKSGTSPK 427

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
              ||||||||:||||| |||||||| |||||||:|||| ||||||||  ||||||||||
Db        428 RWIYDTSKVASGVPYRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 487

Qy        240 IK 241
              :|
Db        488 LK 489


RESULT 15
US-09-798-689-21
; Sequence 21, Application US/09798689
; Patent No. 6811779
; GENERAL INFORMATION:
;  APPLICANT:  Rockwell, Patricia
;  APPLICANT:  Goldstein, Neil I.
;  TITLE OF INVENTION:  Method for Reducing Tumor Growth with VEGF Antagonists
;  TITLE OF INVENTION:  Combined With Radiation and Chemotherapy
;  FILE REFERENCE:  Sequence Listings 1-41  for 381-25 CIP
; Patent No. 6811779
;  CURRENT APPLICATION NUMBER: US/09/798,689
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER:  09/401,163
;  PRIOR FILING DATE:  1999-09-22
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;  PRIOR APPLICATION NUMBER:  08/967,113
;  PRIOR FILING DATE:  1997-11-10
;  PRIOR APPLICATION NUMBER:  08/706,804
;  PRIOR FILING DATE:  1996-09-03
;  PRIOR APPLICATION NUMBER:  08/476,533
;  PRIOR FILING DATE:  1995-06-07
;  PRIOR APPLICATION NUMBER:  08/326,552
;  PRIOR FILING DATE:  1994-10-20
;  PRIOR APPLICATION NUMBER:  08/196,041
;  PRIOR FILING DATE:  1994-02-10
;  NUMBER OF SEQ ID NOS:  41
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 238
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-798-689-21

  Query Match             71.2%;  Score 908;  DB 2;  Length 238;
  Best Local Similarity   74.0%;  Pred. No. 5.4e-66;
  Matches  179;  Conservative   17;  Mismatches   40;  Indels    6;  Gaps    2;

Qy          2 QVQLQQSGPELEKPGASVKLSCKASGYSFTGYTMNWVKQSHGKSLEWIGLITPYNGASSY 61
              ||:||||| ||   ||||||||  ||::   : |:||||   : |||||  |  |  ||  |  |
Db          1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60

Qy         62 NQKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCAR--GGYDGRGFDYWGQGTTVTVS 119
                ||:||||:|  |  ||:|||: |  |||||||:|||:|     |  |:|     ||||||||||||
Db         61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEG----YWGQGTTVTVS 116

Qy        120 SGVGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPK 179
              ||  |||||||||||||||||||||||||||||:|||||||||||||:|||  |||||
Db        117 SGGGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPK 176

Qy        180 RWIYDTSKLASGVPGRFSGSGSGNSYSLTISSVEAEDDATYYCQQWSGYPLTFGAGTKLE 239
               |||  ||  ||||||  ||||||||  |||||||  :||||  |||||||  |  ||  |||:|||||
Db        177 LWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLE 236

Qy        240 IK 241
              ||
Db        237 IK 238


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